

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 17:30:12 ; Search time 919 Seconds

(without alignments)
11440.109 Million cell updates/sec

Title: US-10-689-742-159

Perfect score: 1776
Sequence: 1 agctcacagtgcgcggcg.....ctgtgaaaaaaaaaaaaaa 1776

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1776	100.0	1776	2	AA333810 Coding se
2	1764.4	99.3	1841	3	Aa65072 Membrane-
3	1764.4	99.3	1841	4	Aac91561 Human PRO
4	1764.4	99.3	1841	4	Aas21472 Human cDN
5	1764.4	99.3	1841	4	Aas46225 Human DNA
6	1764.4	99.3	1841	5	Aaf44218 Human PRO
7	1764.4	99.3	1841	5	Abi88154 Human PRO
8	1764.4	99.3	1841	6	Abi95643 Human ang
9	1764.4	99.3	1841	8	ACA89675 Human enco
10	1764.4	99.3	1841	8	ACA73685 Human sec
11	1764.4	99.3	1841	8	ACA06000 Human sec
12	1764.4	99.3	1841	8	ACA66834 cDNA enco
13	1764.4	99.3	1841	8	AC64371 Novel hum
14	1764.4	99.3	1841	8	Acf20409 Human sec
15	1764.4	99.3	1841	8	Acf19795 Human sec
16	1764.4	99.3	1841	8	Ac222083 Human sec
17	1764.4	99.3	1841	8	Acf13248 Human sec
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24	1764.4	99.3	1841	8	ACD18442 Human sec
25	1764.4	99.3	1841	8	ACD08449 Human sec
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39	1764.4	99.3	1841	8	ACC88729 Human sec
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ALIGNMENTS

RESULT 1

AA333810

ID AA333810 standard; DNA; 1776 BP.

XX AC AA333810;

DT 25-JUN-1999 (first entry)

XX DE Coding sequence for human secreted protein bn97_1.

XX KW Secreted protein; human; nutritional activity; cytokine; tissue growth;
XX KW cell proliferation; cell differentiation; immune stimulant; chemotaxis;
XX KW immune suppressant; haematopoiesis regulator; activin; inhibin; cadherin;
XX KW chemokinesis; haemostasis; thrombolysis; anti-inflammatory; gene therapy;
XX KW tumour invasion suppressor; tumour inhibitor; ss.

XX OS Homo sapiens.

XX FN WO9913066-A1.

XX PD 18-MAR-1999.

XX PF 08-SEP-1998; 98WO-US018724.

XX PR 08-SEP-1997; 97US-00929007.

XX PA (GENY) GENETICS INST INC.

XX PI Jacobs K, McCoy JM, Lavallie ER, Racie LA, Evans C, Merberg D;

XX PT Treacy M, Agostino MJ, Spaulding V;

XX DR WPI; 1999-229235/19.

XX DR P-PSDB; AAY05317.

XX PT New polynucleotides encoding secreted human proteins.

XX PS Claim 1; Page 78; 96pp; English.

XX CC This sequence encodes a human secreted protein of the invention. The
XX CC secreted proteins were obtained from human adult placenta, foetal brain,
XX CC adult testes or adult blood cDNA libraries. The polynucleotides (PNS) and
XX CC proteins are predicted to have biological activities which would make
XX CC them suitable for treating, preventing or ameliorating medical conditions

in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The PNs are also stated to be useful for gene therapy

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Query Match      100.0%; Score 1776; DB 2; Length 1776;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Qy	121	CCACCATGAGCTGTCAATTCTCAAGCCTCTGCCACAACCTCGGCATPCAGAGCCCCGGCGCA	180
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Qy	481	CAGACAATGGAAATGGCATGGAGACAAATCTCTACCAAGTCTATAAAGACGACAAAGTT	540
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XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW Pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX Homo sapiens.
OS WO9963088-A2.
PN XX
XX PD
XX 09-DEC-1999.
XX 02-JUN-1999; 99WO-US012252.
XX 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087603P.
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PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.

PR 16-SEP-1998; 98US-0100634P.
XX 12-JAN-1999; 99US-0115565P.
PA (GETH) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
XX WPI; 2000-072883/06.
DR P-PSDB; AAY66728.
XX
PT Membrane-bound proteins and related nucleotide sequences.
XX
XX Claim 2; Fig 229; 822pp; English.
XX
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX
SQ Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;
Query Match 99.3%; Score 1764.4; DB 3; Length 1841;
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;
Matches 1765; Conservative 0;
1 AGCTCACAGTAGCCCGCGGCCCGGCAATCCGACCAATTCATCTCACCGCTGTAG 60
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136 GAATCCAGATGAGGCCCAAGTACAGCAGCAGAGGACATGCTGGATGATGAGGACA 195
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196 CCACCATGAGCCTGATCTCAAGCCTCTGCCAAGCTCGGCATCCAGAGCCCGGCGCA 255
181 CAGAGCAGAGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCTGTGACTTTGT 240
256 CAGAGCAGAGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCTGTGACTTTGT 315
241 GCTTGGTCTGCTGATAGGCTGGCAGCCCTGGGGCTTTTGTCTTTCAGTACTACGAC 300
316 GCTTGGTCTGCTGATAGGCTGGCAGCCCTGGGGCTTTTGTCTTTCAGTACTACGAC 375
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481 CAGAACATGGAATGGCATGGAGCAATTTGCTACAGTTCTATAAAGACAGCAAAAGTT 540
556 CAGAACATGGAATGGCATGGAGCAATTTGCTACAGTTCTATAAAGACAGCAAAAGTT 615
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RESULT 3

AAC91561
ID AAC91561 standard; cDNA; 1841 BP.

XX

AC AAC91561;

DT 21-MAR-2001 (first entry)

XX

DE Human PRO1131 cDNA.

XX

KW Human; PRO; cytostatic; neurotropic; neuroprotective; respiratory general;
antitumor; antitumor; antitumor; antitumor; antitumor; antitumor; antitumor;
PRO agonist; cancer; inflammatory disorder; immunosuppressive; immunostimulant;
PRO agonist; cancer; inflammatory disorder; immunosuppressive; immunostimulant; ss.

XX

OS Homo sapiens.

XX

PN WO200073348-A2.

XX

PD 07-DEC-2000.

XX

XX

PF 30-MAY-2000; 2000WO-US014941.

XX

PR 02-JUN-1999; 99WO-US012252.

PR 22-JUN-1999; 99US-0140650P.

PR 23-JUN-1999; 99US-014037P.

PR 20-JUL-1999; 99US-0144758P.

PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.

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PR 09-DEC-1999; 99US-0170262P.

PR 16-DEC-1999; 99WO-US030095.

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PR 15-MAR-2000; 2000WO-US006884.

PR 30-MAR-2000; 2000WO-US008439.

PR 17-MAY-2000; 2000WO-US013705.

XX

XX

PA (GETH) GENENTECH INC.

XX

PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;

PI Shelton DL, Smith V, Watanabe CK, Wood WI;

XX

XX

DR WPI; 2001-016509/02.

DR P-PSDB; AAB50959.

XX

XX

PT Twenty eight nucleic acids encoding PRO polypeptides which are useful for

PT treating various tumors, e.g. breast cancer, and other inflammatory,

PT angiogenic and immunological disorders.

XX

XX

PS Claim 20; Fig 17; 188pp; English.

XX

XX

CC The present sequence is one of twenty eight nucleic acids encoding PRO

CC polypeptides. The PRO polypeptides and their agonists, including

XX

XX

CC

CC antibodies, peptides, and small molecule agonists, may be used to treat
CC various tumors, e.g., cancers such as breast cancer, ovarian cancer,
CC renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung
CC cancer, bladder cancer, central nervous system cancer, melanoma or
CC leukemia. They are also useful for treating other disorders such as
CC neuronal, glial, astrocytic, hypothalamic and other glandular,
CC macrophage, epithelial, stromal and blastocoele disorders, and
CC inflammatory, angiogenic and immunological disorders
XX
SQ Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;

Query Match 99.3%; Score 1764.4; DB 4; Length 1841;
Best Local Similarity 99.9%; Pred No. 0;
Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGCTCAGTAGCCCGCGGCCAGGGCAATCCGACCACTTCACTCTCACCGCTGTAG 60
Db 76 AGCTCAGTAGCCCGCGGCCAGGGCAATCCGACCACTTCACTCTCACCGCTGTAG 135
QY 61 GAATCCAGATGAGGCGCAAGTACAGCAGCAGGAGCATGCTGGATGATGAGGACA 120
Db 136 GAATCCAGATGAGGCGCAAGTACAGCAGCAGGAGCATGCTGGATGATGAGGACA 195
QY 121 CCACCATGAGCTGCATTCTCAAGCTCTGCCACAACCTCGCATCCAGAGCCCGCGCA 180
Db 196 CCACCATGAGCTGCATTCTCAAGCTCTGCCACAACCTCGCATCCAGAGCCCGCGCA 255
QY 181 CAGAGCAGAGGCTCCCTCTTCAAGCTGGCGCAGAGTGGCCCTGACCTCTGCTGCTTGT 240
Db 256 CAGAGCAGAGGCTCCCTCTTCAAGCTGGCGCAGAGTGGCCCTGACCTCTGCTGCTTGT 315
QY 241 GCTTGGTCTGCTGATAGGCTGGCAGCCCTGGGGCTTTTGTCTTTCAGTACTACGAGC 300
Db 316 GCTTGGTCTGCTGATAGGCTGGCAGCCCTGGGGCTTTTGTCTTTCAGTACTACGAGC 375
QY 301 TCTCAATGCTGCTCAAGACACCACTTCTCAATGGAAGAAAGATTAGAAATAGTCCC 360
Db 376 TCTCAATGCTGCTCAAGACACCACTTCTCAATGGAAGAAAGATTAGAAATAGTCCC 435
QY 361 AAGAGTTGCAATCTCTTCAAGTCCAGATATAAAGCTTGCAGGAAGTCTGCAGCATGTGG 420
Db 436 AAGAGTTGCAATCTCTTCAAGTCCAGATATAAAGCTTGCAGGAAGTCTGCAGCATGTGG 495
QY 421 CTGAAAACTCTGCTGAGCTGTATATAAAGCTGGAGCACAAGGTGAGCCCTTGTGA 480
Db 496 CTGAAAACTCTGCTGAGCTGTATATAAAGCTGGAGCACAAGGTGAGCCCTTGTGA 555
QY 481 CAGAACATGGAATGCGATGCGATGCAATGCTACCACTTCTATAAAGCAGCAAAAGTT 540
Db 556 CAGAACATGGAATGCGATGCGATGCAATGCTACCACTTCTATAAAGCAGCAAAAGTT 615
QY 541 GGGAGGACTGTAAATATTTCTGCGCTTGTGAAAACTCTACCATGCTGAAGATAAACAAC 600
Db 616 GGGAGGACTGTAAATATTTCTGCGCTTGTGAAAACTCTACCATGCTGAAGATAAACAAC 675
QY 601 AAGAAGACCTGGAATTTGCGCGCTCTCAGAGTACTCTGAGTCTTCTTCTTATTGA 660
Db 676 AAGAAGACCTGGAATTTGCGCGCTCTCAGAGTACTCTGAGTCTTCTTCTTATTGA 735
QY 661 CAGGCTTTTGGCGCTGACAGTGGCAGGCTGCTGCTGGATGATGAGAACCCCTTTCA 720
Db 736 CAGGCTTTTGGCGCTGACAGTGGCAGGCTGCTGCTGGATGATGAGAACCCCTTTCA 795
QY 721 CTTCTGAACTGTTCCATATTAATAGATGTCAACAGCCCAAGAGCAGAGACTGTGTGG 780
Db 796 CTTCTGAACTGTTCCATATTAATAGATGTCAACAGCCCAAGAGCAGAGACTGTGTGG 855
QY 781 CCATCTTAAATGGGATGATCTTCTCAAGAGACTGCAAGAAATTAAGCGTTGTGTGTG 840
Db 856 CCATCTTAAATGGGATGATCTTCTCAAGAGACTGCAAGAAATTAAGCGTTGTGTGTG 915
QY 841 AAGAAGGCGAGGAATGTTGAGGCGCAGAGCCCTCCATGTCCTCCCTGAACATTTAGGG 900

CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 2/5 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;

Query Match 99.3%; Score 1764.4; DB 4; Length 1841;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTCACAGTAGCCCGCGCCAGGCGCAATCGACACATTTCACTCTCACCGCTGTAG 60
DB |||||
DB 76 AGCTCACAGTAGCCCGCGCCAGGCGCAATCGACACATTTCACTCTCACCGCTGTAG 135
QY 61 GAATCCAGATGCGAGGCGCAAGTACAGCAGCACGAGGAGCATGCTGGATGATGAGGGACA 120
DB |||||
DB 136 GAATCCAGATGCGAGGCGCAAGTACAGCAGCACGAGGAGCATGCTGGATGATGAGGGACA 195
QY 121 CCACCATGAGCCTGCAATCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCGCGCA 180
DB |||||
DB 196 CCACCATGAGCCTGCAATCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCGCGCA 255
QY 181 CAGAGCACAGGGCTCCCTCTTCAAGCTGGCGACAGCTGCCCTGACCTGCTGACTTGT 240
DB |||||
DB 256 CAGAGCACAGGGCTCCCTCTTCAAGCTGGCGACAGCTGCCCTGACCTGCTGACTTGT 315
QY 241 GCTTGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTCAGTACTACCAGC 300
DB |||||
DB 316 GCTTGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTCAGTACTACCAGC 375
QY 301 TCTCCAACTACTGGTCAAGACACATTTCTCAATGGAAGAAAGATTAGGAATAGCTCCC 360
DB |||||
DB 376 TCTCCAACTACTGGTCAAGACACATTTCTCAATGGAAGAAAGATTAGGAATAGCTCCC 435
QY 361 AAGAGTTGCAATCTCTTCAAGTCCAGATATAAAGCTTCAGGAAGCTTCGACGACTGG 420
DB |||||
DB 436 AAGAGTTGCAATCTCTTCAAGTCCAGATATAAAGCTTCGAGGAAGCTTCGACGACTGG 495
QY 421 CTGAAAACCTCTGTCTGAGCTGTATACAAAGCTGGAGCACACAGGTGACGCCCTTGTA 480
DB |||||
DB 496 CTGAAAACCTCTGTCTGAGCTGTATACAAAGCTGGAGCACACAGGTGACGCCCTTGTA 555
QY 481 CAGAACATGGAATGGGCAATGGGCAATTTCTCAATGGAAGAAAGATTAGGAATAGCTCCC 540
DB |||||
DB 556 CAGAACATGGAATGGGCAATGGGCAATTTCTCAATGGAAGAAAGATTAGGAATAGCTCCC 615
QY 541 GGGAGGACTGTAATATTTCTGCTTGTAGTGAACCTCTACCATGCTGAGAGATAAACAAC 600
DB |||||
DB 616 GGGAGGACTGTAATATTTCTGCTTGTAGTGAACCTCTACCATGCTGAGAGATAAACAAC 675
QY 601 AAGAAGACCTGGAATTTGGCGGCTCTCAGAGCTACTCTGAGTGTCTTCTCTTATTGGA 660
DB |||||
DB 676 AAGAAGACCTGGAATTTGGCGGCTCTCAGAGCTACTCTGAGTGTCTTCTCTTATTGGA 735
QY 661 CAGGGCTTTTGGCCCTGACAGTGGCAAGCCCTGGCTGTGGATGGAGAACCCCTTTCA 720
DB |||||
DB 736 CAGGGCTTTTGGCCCTGACAGTGGCAAGCCCTGGCTGTGGATGGAGAACCCCTTTCA 795
QY 721 CTTCTGAACTGTTCATATTAATAGATGTCCACAGCCCAAGAGCAGAGACTGTGG 780
DB |||||

RESULT 5
AAS46225

DB 796 CTTCTGAACTGTTCCATATTATATAGATGTCCACAGCCCAAGAGCAGAGACTGTGTGG 855
QY 781 CCATCTCTTAATGGAGTATCTTCTCAAGAGACTGCAAGAAATGAGCGTGTGTCTGTG 840
DB 856 CCATCTCTCAATGGAGTATCTTCTCAAGAGACTGCAAGAAATGAGCGTGTGTCTGTG 915
QY 841 AGAGAGGCGCAGGAATGGTGAAGCAGAGAGCCTCCATGTGCTCCCTGAAACATTTAGGCG 900
DB 916 AGAGAGGCGCAGGAATGGTGAAGCAGAGAGCCTCCATGTGCTCCCTGAAACATTTAGGCG 975
QY 901 AAGGTGACTGATTCGCCCTCTCCAACTACAAATAGCAGAGTGAAGCGGCTGCCAAG 960
DB 976 AAGGTGACTGATTCGCCCTCTCCAACTACAAATAGCAGAGTGAAGCGGCTGCCAAG 1035
QY 961 CAAGGGCTAGTTGAGACATTTGGAAATGGAACATTAATCAGGAAAGACTATCTCTGACT 1020
DB 1036 CAAGGGCTAGTTGAGACATTTGGAAATGGAACATTAATCAGGAAAGACTATCTCTGACT 1095
QY 1021 AGTACAAATGGGTTCTGCTGTTTCTGTTCAAGATCACCAGCATTTCTGAGCTTGGGT 1080
DB 1096 AGTACAAATGGGTTCTGCTGTTTCTGTTCAAGATCACCAGCATTTCTGAGCTTGGGT 1155
QY 1081 TATGACAGTATTTAAACAGTCAACAAGAGTCTTTATTTACATGCGCACCAACCACTCAGAA 1140
DB 1156 TATGACAGTATTTAAACAGTCAACAAGAGTCTTTATTTACATGCGCACCAACCACTCAGAA 1215
QY 1141 ACCCATATGTCATCTGCTTCTTGGCTTAGAGATAAATTTTGTAGTCTCTCTTCTCAA 1200
DB 1216 ACCCATATGTCATCTGCTTCTTGGCTTAGAGATAAATTTTGTAGTCTCTCTTCTCAA 1275
QY 1201 TGTCTAATATCACCTCCCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTT 1260
DB 1276 TGTCTAATATCACCTCCCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTT 1335
QY 1261 TTGAAGTAGAGGAAATACATTTGAGTAACTCCTTTTCTGACAGTCAAGTAGTCCATC 1320
DB 1336 TTGAAGTAGAGGAAATACATTTGAGTAACTCCTTTTCTGACAGTCAAGTAGTCCATC 1395
QY 1321 AGAAATGGCAGTCACTTCCAGATTTGTAACAGAAATACACAGAAATTTCTTTTGT 1380
DB 1396 AGAAATGGCAGTCACTTCCAGATTTGTAACAGAAATACACAGAAATTTCTTTTGT 1455
QY 1381 GTTTCAGTTTCATCTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTGTCCA 1440
DB 1456 GTTTCAGTTTCATCTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTGTCCA 1515
QY 1441 TGCCGTTTCCCAACAGGAGTGTCACTTCATATGAAATCTCAAAATCTCAATGCCTTATAA 1500
DB 1516 TGCCGTTTCCCAACAGGAGTGTCACTTCATATGAAATCTCAAAATCTCAATGCCTTATAA 1575
QY 1501 GCATTCCTTCTGTCCTCAATTAAGACTCTGATAATTTGTTCTCCCTCCATAGGAAATTTCTC 1560
DB 1576 GCATTCCTTCTGTCCTCAATTAAGACTCTGATAATTTGTTCTCCCTCCATAGGAAATTTCTC 1635
QY 1561 CCAGGAAAGAAATATATCCCATCTCCGTTTTCATATCAGAACTACCGTCCCGATATTC 1620
DB 1636 CCAGGAAAGAAATATATCCCATCTCCGTTTTCATATCAGAACTACCGTCCCGATATTC 1695
QY 1621 CTTTCAGAGAGATTAAGACACAGAAAGTGTAGCCTCTTCTCTGACCTGTAAATAGTTT 1680
DB 1696 CTTTCAGAGAGATTAAGACACAGAAAGTGTAGCCTCTTCTCTGACCTGTAAATAGTTT 1755
QY 1681 CAGTTCCTTATTTCTTCCATTTGACCCATTTATTTATACCTTTTTCAGGTAATTAATA 1740
DB 1756 CAGTTCCTTATTTCTTCCATTTGACCCATTTATTTATACCTTTTTCAGGTAATTAATA 1815
QY 1741 ATAATAATGTAAATACTGTGAAAAA 1766
DB 1816 ATAATAATGTAAATACTGTGAAAAA 1841

ID AAS46225 standard; cDNA; 1841 BP.
XX AC AAS46225;
XX DT 18-DEC-2001 (first entry)
XX DE Human DNA encoding PRO polypeptide sequence #301.
XX KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX OS Homo sapiens.
XX PN WO200168848-A2.
XX PD 20-SEP-2001.
XX PF 28-FEB-2001; 2001WO-US006520.
XX PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
PR 15-MAR-2000; 2000US-0189328P.
PR 14-MAR-2000; 2000US-0189328P.
PR 21-MAR-2000; 2000US-0006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194449P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000WO-US013705.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX (GETH) GENENTECH INC.
XX PA Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2001-602746/68.
XX P-PSDB; AAU29324.
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.

XX Claim 2; Fig 601; 774pp; English.
XX PS Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX SQ Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;
Query Match 99.3%; Score 1764.4; DB 4; Length 1841;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGCTCACAGTAGCCGGCGGCCAGGGCAATCCGACCACATTTCACTCTCACCGCTGTAG 60
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
76 AGCTCACAGTAGCCGGCGGCCAGGGCAATCCGACCACATTTCACTCTCACCGCTGTAG 135
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 GAATCCAGATGACGGCCAAAGTACAGCAGCAGCGGACATCTGGATGATGATGGGACA 120
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
136 GAATCCAGATGACGGCCAAAGTACAGCAGCAGCGGACATCTGGATGATGATGGGACA 195
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 CCACATGAGCTGCATTTCTCAAGCTCTGCCACACTCGGCATCCAGAGCCCGCGCGCA 180
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
196 CCACATGAGCTGCATTTCTCAAGCTCTGCCACACTCGGCATCCAGAGCCCGCGCGCA 255
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 CAGAGCACAGGGCTCCCTCTTCAAGCTGGCGACAGTGGCCCTGACCTCTGCTACTTTGT 240
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
256 CAGAGCACAGGGCTCCCTCTTCAAGCTGGCGACAGTGGCCCTGACCTCTGCTACTTTGT 315
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 GCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTGTTTTCAGTACTACCCAGC 300
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
316 GCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTGTTTTCAGTACTACCCAGC 375
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 TCTCCATACCTGGTCAAGACACCAATTTCTCAATGGAGAGAGATTAGGAATAGTCCC 360
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
376 TCTCCATACCTGGTCAAGACACCAATTTCTCAATGGAGAGAGATTAGGAATAGTCCC 435
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 AAGAGTTGCAATCTCTTCAAGTCCAGATATAAAGCTTGCAGGAAGTCTGCAGCATGTGG 420
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
436 AAGAGTTGCAATCTCTTCAAGTCCAGATATAAAGCTTGCAGGAAGTCTGCAGCATGTGG 495
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 CTGAAAAACTCTGTGTGAGCTGTATATAAAGCTGGAGCACAAGTGTGAGCCCTTGTGA 480
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
496 CTGAAAAACTCTGTGTGAGCTGTATATAAAGCTGGAGCACAAGTGTGAGCCCTTGTGA 555
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 CAGAACATGGAATGGCATGGAGACATTTGCTACCAGTTCTATAAACAGCAGCAAGTT 540
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
556 CAGAACATGGAATGGCATGGAGACATTTGCTACCAGTTCTATAAACAGCAGCAAGTT 615
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 GGGAGGACTGTAATATTTCTGCCCTTAGTAAAACTCTACCATGCTGAAGATAAAACAAC 600
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
616 GGGAGGACTGTAATATTTCTGCCCTTAGTAAAACTCTACCATGCTGAAGATAAAACAAC 675
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 AAGAAGACCTCGAATTTGCCCGCTCTCAGAGCTACTCTGAGTTTCTTCTTATTTGA 660
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
676 AAGAAGACCTCGAATTTGCCCGCTCTCAGAGCTACTCTGAGTTTCTTCTTATTTGA 735
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 CAGGGCTTTTGGCGCCCTGACAGTGGCAGGCTGGCTGTGGATGGATGGAAACCCCTTTCA 720
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
736 CAGGGCTTTTGGCGCCCTGACAGTGGCAGGCTGGCTGTGGATGGATGGAAACCCCTTTCA 795

QY 721 CTTCTGAATGTTCCATATTATAATAGATGTCCACAGCCCAAGACAGAGACTGTGTGG 780
DB 796 CTTCTGAATGTTCCATATTATAATAGATGTCCACAGCCCAAGACAGAGACTGTGTGG 855
QY 781 CCATCCTTAATGGATGATCTTCTCAAGAGATGCAAGAAATTTGAAGCGTTGTGTCTGTG 840
DB 856 CCATCCTTAATGGATGATCTTCTCAAGAGATGCAAGAAATTTGAAGCGTTGTGTCTGTG 915
QY 841 AGAAGAGGAGAGATGTTGAAGCCAGAGAGCTCCATGTCCCTCCCTGAAACATTAGGGG 900
DB 916 AGAAGAGGAGAGATGTTGAAGCCAGAGAGCTCCATGTCCCTCCCTGAAACATTAGGGG 975
QY 901 AAGGTGACTGATTCGCTCTGCACTACAAATAGCAGAGTGCAGCCAGCGGTGCCAAG 960
DB 976 AAGGTGACTGATTCGCTCTGCACTACAAATAGCAGAGTGCAGCCAGCGGTGCCAAG 1035
QY 961 CAAGGGCTAGTTGAGACATTTGGAAATGGAACATATCAGGAAAGACTATCTCTCTGACT 1020
DB 1036 CAAGGGCTAGTTGAGACATTTGGAAATGGAACATATCAGGAAAGACTATCTCTCTGACT 1095
QY 1021 AGTACAAAATGGGTTCTGTGTTTCTGTTCAGGATCAACAGATTTCTGAGCTTGGGTT 1080
DB 1096 AGTACAAAATGGGTTCTGTGTTTCTGTTCAGGATCAACAGATTTCTGAGCTTGGGTT 1155
QY 1081 TATGCAAGTATTTAAGTCAAGAGTCTTATTTACATGCCCAACCAACCTCAGAA 1140
DB 1156 TATGCAAGTATTTAAGTCAAGAGTCTTATTTACATGCCCAACCAACCTCAGAA 1215
QY 1141 ACCATAAATGTCATCTGCTCTTCTGCTTAGAGATAAATTTTAGCTCTCTTCTCTCAA 1200
DB 1216 ACCATAAATGTCATCTGCTCTTCTGCTTAGAGATAAATTTTAGCTCTCTTCTCTCAA 1275
QY 1201 TGTCTAATATCACTCCCTGTTTTCATGTTCTTCTTACACTTGGTGAATAAGAACTTTT 1260
DB 1276 TGTCTAATATCACTCCCTGTTTTCATGTTCTTCTTACACTTGGTGAATAAGAACTTTT 1335
QY 1261 TTGAGTAGAGGAATATAGGTAAATCTCTTCTGACAGTCAAGTAGTCCATC 1320
DB 1336 TTGAGTAGAGGAATATAGGTAAATCTCTTCTGACAGTCAAGTAGTCCATC 1395
QY 1321 AGAATTTGGCAGTCACTTCCAGATTTGACAGCAATACACAGGAATTTCTTTTGTGT 1380
DB 1396 AGAATTTGGCAGTCACTTCCAGATTTGACAGCAATACACAGGAATTTCTTTTGTGT 1455
QY 1381 GTTTCAGTTTATCTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTGTCCA 1440
DB 1456 GTTTCAGTTTATCTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTGTCCA 1515
QY 1441 TGCCGTTTCCCAACAGGATGTCACTTGATATGAGAAATCTCAATCTCAATGCTTATAA 1500
DB 1516 TGCCGTTTCCCAACAGGATGTCACTTGATATGAGAAATCTCAATCTCAATGCTTATAA 1575
QY 1501 GCATTCCTTCTGTGTCCATTAAGACTCTGATAATTTGTCTCCCTCCATAGGAATTTCTC 1560
DB 1576 GCATTCCTTCTGTGTCCATTAAGACTCTGATAATTTGTCTCCCTCCATAGGAATTTCTC 1635
QY 1561 CCAGGAAGAAATATATCCCATCTCCGTTTTCATATCAGAACTACCGTCCCGATATCC 1620
DB 1636 CCAGGAAGAAATATATCCCATCTCCGTTTTCATATCAGAACTACCGTCCCGATATCC 1695
QY 1621 CTTTCAGAGATTTAAGACAGAAAAAGTGAAGCTCTTTCATCTGCACTGTAAATAGTTT 1680
DB 1696 CTTTCAGAGATTTAAGACAGAAAAAGTGAAGCTCTTTCATCTGCACTGTAAATAGTTT 1755
QY 1681 CAGTTCTCTATTTCTTCCATTCAGCCCATATTTATCTTCTGAGTCAAGATTATAA 1740
DB 1756 CAGTTCTCTATTTCTTCCATTCAGCCCATATTTATCTTCTGAGTCAAGATTATAA 1815
QY 1741 ATAATAAATGTAATACTGTGAAAA 1766
DB 1816 ATAATAAATGTAATACTGTGAAAA 1841

RESULT 6

AAF44218

ID AAF44218 standard; cDNA; 1841 BP.

XX

AC AAF44218;

XX

DT 02-APR-2001 (first entry)

XX

DE Human PRO1131 (UNQ569) nucleotide sequence SEQ ID NO:318.

XX

KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
cancer; chromosomal mapping; gene mapping; tissue typing;
diagnostic assay; ss.

XX

OS Homo sapiens.

XX

PN WO200073454-A1.

XX

PD 07-DEC-2000.

XX

PF 30-MAR-2000; 2000WO-US008439.

XX

PR 02-JUN-1999; 99WO-US012252.

XX

PR 23-JUN-1999; 99US-0141037P.

XX

PR 07-JUL-1999; 99US-0143048P.

XX

PR 20-JUL-1999; 99US-0144758P.

XX

PR 26-JUL-1999; 99US-0145698P.

XX

PR 28-JUL-1999; 99US-0146222P.

XX

PR 17-AUG-1999; 99US-0149396P.

XX

PR 15-SEP-1999; 99WO-US021090.

XX

PR 15-SEP-1999; 99WO-US021547.

XX

PR 08-OCT-1999; 99US-0158663P.

XX

PR 30-NOV-1999; 99WO-US028313.

XX

PR 01-DEC-1999; 99WO-US028301.

XX

PR 16-DEC-1999; 99WO-US030095.

XX

PR 20-DEC-1999; 99WO-US030911.

XX

PR 05-JAN-2000; 2000WO-US000219.

XX

PR 06-JAN-2000; 2000WO-US000376.

XX

PR 11-FEB-2000; 2000WO-US003565.

XX

PR 18-FEB-2000; 2000WO-US004341.

XX

PR 22-FEB-2000; 2000WO-US004914.

XX

PR 24-FEB-2000; 2000WO-US005004.

XX

PR 02-MAR-2000; 2000WO-US005841.

XX

PR 15-MAR-2000; 2000WO-US006884.

XX

PR 20-MAR-2000; 2000WO-US007377.

XX

(GETH) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

XX

PI Ferrara N, Fong S, Gerber H, Grittisen ME, Goddard A, Godowski PJ;

XX

PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;

XX

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;

XX

PI Zhang Z;

DR WPI; 2001-032160/04.

XX

DR P-PSDB; AAB65251.

XX

PT PRO polynucleotides used to produce polypeptides used to target bioactive
molecules such as toxins, radiolabels or antibodies, to specific cells,
to cause targeted cell death.

XX

PS Claim 2; Fig 229; 935pp; English.

XX

CC The present invention describes human secreted and transmembrane PRO
proteins. The PRO proteins have cytostatic activity. The PRO proteins can
be used for targeted delivery of bioactive molecules, such as toxins,
radiolabels or antibodies, that cause cell death. PRO nucleotide
sequences, and their fragments, can be used as hybridisation probes, in
chromosomal and gene mapping, and in the generation of anti-sense RNA and
DNA. They may also be used to produce transgenic animals which are used
to develop and screen therapeutically useful reagents. The PRO nucleotide

CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAF65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention

XX
SQ Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;
Query Match 99.3%; Score 1764.4; DB 5; Length 1841;
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;
Matches 1765; Conservative 0;
QY 1 AGCTCACAGTAGCCCGGGCCAGGCAATCCGACCAATTCACCTCTCACCGCTGTAG 60
DB 76 AGCTCACAGTAGCCCGGGCCAGGCAATCCGACCAATTCACCTCTCACCGCTGTAG 135
QY 61 GAATCCAGATGAGGCCAAGTACAGCAGCAGGAGCATGCTGATGATGATGGGACA 120
DB 136 GAATCCAGATGAGGCCAAGTACAGCAGCAGGAGCATGCTGATGATGATGGGACA 195
QY 121 CCACATGAGCCTGATTCACAGCTCTCAAGCTCTGCCACAACCTCGGCATCCAGGCCCGGCGCA 180
DB 196 CCACATGAGCCTGATTCACAGCTCTCAAGCTCTGCCACAACCTCGGCATCCAGGCCCGGCGCA 255
QY 181 CAGAGCACAGGCGCTCCCTCTTCAAGCTGGCGACAGTGGCCCTGACCCCTGCTGACTTTGT 240
DB 256 CAGAGCACAGGCGCTCCCTCTTCAAGCTGGCGACAGTGGCCCTGACCCCTGCTGACTTTGT 315
QY 241 GCTTGGTGTCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTGTTTTTCACTACTACCGC 300
DB 316 GCTTGGTGTCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTGTTTTTCACTACTACCGC 375
QY 301 TCTCCAATAGTCTCAAGTCCAGACCAATTTCTCAATGGAGAGATTTAGGAATAGTCCC 360
DB 376 TCTCCAATAGTCTCAAGTCCAGACCAATTTCTCAATGGAGAGATTTAGGAATAGTCCC 435
QY 361 AAGAGTGTCAATCTCTTCAAGTCCAGATATAAAGCTTGCAGGAAGTCTGCAGCATGTGG 420
DB 436 AAGAGTGTCAATCTCTTCAAGTCCAGATATAAAGCTTGCAGGAAGTCTGCAGCATGTGG 495
QY 421 CTGAAAAACTCTGCTGAGCTGTATATAAAGCTTGGAGCACACAGGTGCGAGCCCTTGT 480
DB 496 CTGAAAAACTCTGCTGAGCTGTATATAAAGCTTGGAGCACACAGGTGCGAGCCCTTGT 555
QY 481 CAGACAATGGAATGGCATGGAGCAATTCCTACAGTCTCTATAAGACGACGCAAAAGTT 540
DB 556 CAGACAATGGAATGGCATGGAGCAATTCCTACAGTCTCTATAAGACGACGCAAAAGTT 615
QY 541 GGGAGGACTGTAAATATTTCTGCCCTTAGTGAATACTTACCATGCTGAAGATAAACAAC 600
DB 616 GGGAGGACTGTAAATATTTCTGCCCTTAGTGAATACTTACCATGCTGAAGATAAACAAC 675
QY 601 AAGAAGACTGGAATTTGGCGGTCTCAGAGTACTCTGAGTTTTTCTACTTTATTTGGA 660
DB 676 AAGAAGACTGGAATTTGGCGGTCTCAGAGTACTCTGAGTTTTTCTACTTTATTTGGA 735
QY 661 CAGGCTTTTGGCCCTGACAGTGGCAAGGCTGCTGTGATGATGATGAACCCCTTTCA 720
DB 736 CAGGCTTTTGGCCCTGACAGTGGCAAGGCTGCTGTGATGATGATGAACCCCTTTCA 795
QY 721 CTTCGAACTGTTCATATTAATAGATGTCCAGGCCCAAGAGCAGAGACTGTGTGG 780
DB 796 CTTCGAACTGTTCATATTAATAGATGTCCAGGCCCAAGAGCAGAGACTGTGTGG 855
QY 781 CCATCTTAAATGGGATGATCTTCTCAAGGACTGCAAGAAATGAAGCGTTGTGTCTGTG 840
DB 856 CCATCTTCAATGGGATGATCTTCTCAAGGACTGCAAGAAATGAAGCGTTGTGTCTGTG 915
QY 841 AGAGAAGGCGAGGAATGTTGAAGCAGAGAGCCTCCATGTCCCCCTGAAACATTTAGGCG 900
DB 916 AGAGAAGGCGAGGAATGTTGAAGCAGAGAGCCTCCATGTCCCCCTGAAACATTTAGGCG 975

QY 901 AAGGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGCGTGCAAG 960
DB 976 AAGGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGCGTGCAAG 1035
QY 961 CAAGGGCTAGTTGAGACATTTGGGAAATGGAACATATCAGGAAGACATCTCTCTGACT 1020
DB 1036 CAAGGGCTAGTTGAGACATTTGGGAAATGGAACATATCAGGAAGACATCTCTCTGACT 1095
QY 1021 AGTACAAATGGGTTCTCGTGTTCCTGTTTCTGAGGATCACCAGCATTTCTGAGCTTGGGTT 1080
DB 1096 AGTACAAATGGGTTCTCGTGTTCCTGTTTCTGAGGATCACCAGCATTTCTGAGCTTGGGTT 1155
QY 1081 TATGACATATTTTAAACAGTCTCAAGAAAGTCTTTATTTACATGCGCAACCAACCTCAGAA 1140
DB 1156 TATGACATATTTTAAACAGTCTCAAGAAAGTCTTTATTTACATGCGCAACCAACCTCAGAA 1215
QY 1141 ACCNATATGTCATCTGCTTCTTGGCTTAGAGATAAATTTTAGTCTCTCTTCTCTCAA 1200
DB 1216 ACCNATATGTCATCTGCTTCTTGGCTTAGAGATAAATTTTAGTCTCTCTTCTCTCAA 1275
QY 1201 TGTCTAATATCACCTCCCTGTTTTCATGCTTCTTACACTTGGTGGAAATGAAGAACTTT 1260
DB 1276 TGTCTAATATCACCTCCCTGTTTTCATGCTTCTTACACTTGGTGGAAATGAAGAACTTT 1335
QY 1261 TTGAAGTAGAGGAAATACATTTGAGGTAAACATCTTCTTCTGACAGTCAAGTAGTCCATC 1320
DB 1336 TTGAAGTAGAGGAAATACATTTGAGGTAAACATCTTCTTCTGACAGTCAAGTAGTCCATC 1395
QY 1321 AGAAATTTGGCAGTCACTTCCAGATTTGACAGCAATAACACAGGAATTTCTTTTGTGTT 1380
DB 1396 AGAAATTTGGCAGTCACTTCCAGATTTGACAGCAATAACACAGGAATTTCTTTTGTGTT 1455
QY 1381 GTTTCAGTTTCACTAGTCCCTTCCCAATCATCAGTAAAGACCCCATCTGCCTTGTCCA 1440
DB 1456 GTTTCAGTTTCACTAGTCCCTTCCCAATCATCAGTAAAGACCCCATCTGCCTTGTCCA 1515
QY 1441 TGCGGTTTCCCAACAGGGATGTCATTTGATATGAGAATCTCAAAATCTCAATGCCTTATAA 1500
DB 1516 TGCGGTTTCCCAACAGGGATGTCATTTGATATGAGAATCTCAAAATCTCAATGCCTTATAA 1575
QY 1501 GCATTCCTTCTGTGTCCATTAAGACTCTGATAATTTGTCTCCCTCCATAGGAATTTCTC 1560
DB 1576 GCATTCCTTCTGTGTCCATTAAGACTCTGATAATTTGTCTCCCTCCATAGGAATTTCTC 1635
QY 1561 CCAGAAAGAAATATATCCCATCTCCGTTTTCATATCAGAACTACCGTCCCGATATTTC 1620
DB 1636 CCAGAAAGAAATATATCCCATCTCCGTTTTCATATCAGAACTACCGTCCCGATATTTC 1695
QY 1621 CTTCAGAGAGATTAAAGACAGAAAAAGTAGGCGCTCTTCTATCTGCACCTGTAAATAGTTT 1680
DB 1696 CTTCAGAGAGATTAAAGACAGAAAAAGTAGGCGCTCTTCTATCTGCACCTGTAAATAGTTT 1755
QY 1681 CAGTTCCTATTTTCTTCCATTTGACCCATATTTTACCTTTTTCAGTACTGAGAAATTAATA 1740
DB 1756 CAGTTCCTATTTTCTTCCATTTGACCCATATTTTATATCTTTCAGGTAAGAAATTAATA 1815
QY 1741 ATAATAAATGATAATACCTGTGAAAAA 1766
DB 1816 ATAATAAATGATAATACCTGTGAAAAA 1841

RESULT 7

ABL88154
ID ABL88154 standard; cDNA; 1841 BP.

XX AC ABL88154;

XX DT 16-MAY-2002 (first entry)

XX DE Human PRO1131 cDNA sequence SEQ ID NO:165.

XX KW Human; angiogenesis; cardiant; cyotostatic; antiangiogenic; hypotensive;
vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;

gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 age-related macular degeneration; arterial restenosis; angina;
 rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 wound healing; chromosome mapping; gene mapping; gene; ss.

XX Homo sapiens.

XX WO200200690-A2.

XX 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-0213637P.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220654P.

XX 28-JUL-2000; 2000WO-US020710.

XX 02-AUG-2000; 2000US-0222695P.

XX 17-AUG-2000; 2000US-00643657.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 07-SEP-2000; 2000US-0230978P.

XX 18-SEP-2000; 2000US-00664610.

XX 18-SEP-2000; 2000US-00665350.

XX 24-OCT-2000; 2000US-0249222P.

XX 08-NOV-2000; 2000US-00709238.

XX 08-NOV-2000; 2000WO-US030952.

XX 10-NOV-2000; 2000WO-US030873.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

XX 22-JAN-2001; 2001US-00767609.

XX 28-FEB-2001; 2001US-00796498.

XX 28-FEB-2001; 2001WO-US008520.

XX 01-MAR-2001; 2001WO-US008666.

XX 09-MAR-2001; 2001US-00802706.

XX 14-MAR-2001; 2001US-00808689.

XX 22-MAR-2001; 2001US-00816744.

XX 05-APR-2001; 2001US-00828366.

XX 10-MAY-2001; 2001US-00854208.

XX 25-MAY-2001; 2001US-00854280.

XX 25-MAY-2001; 2001US-00866028.

XX 25-MAY-2001; 2001US-00866034.

XX 30-MAY-2001; 2001WO-US017092.

XX 30-MAY-2001; 2001US-00870574.

XX 01-JUN-2001; 2001WO-US017443.

(GETH) GENENTECH INC.
 Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 WPI; 2002-090516/12.
 P-PSDB; ABB84899.
 One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 infarction), endothelial or angiogenic disorders in a mammal.
 Claim 2; Fig 165; 565pp; English.
 ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
 antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 activities, and can be used in gene therapy. The PRO polynucleotides,
 proteins, agonists and antagonists are useful for treating or diagnosing
 a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 cardiac hypertrophy, trauma, cancer, age-related macular degeneration,

CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention
 XX

SQ Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;

	Query Match	Best Local Similarity	Score	1764.4;	DB 6;	Length	1841;			
	Matches	1765;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	AGCTCACAGTACCCCGCGGCC	CCAGGGCAATCCGACCACTTCTACCTC	CACCGCTGTAG	60					
DB	76	AGCTCACAGTACCCCGCGGCC	CCAGGGCAATCCGACCACTTCTACCTC	CACCGCTGTAG	135					
QY	61	GAATCCAGATGCAGGCCAAGTACAGCAGCAGCAGGACATGCTGGATGATGATGGGACA	120							
DB	136	GAATCCAGATGCAGGCCAAGTACAGCAGCAGCAGGACATGCTGGATGATGATGGGACA	195							
QY	121	CCACCATGAGCCTGCAATCTCAAGCCTCTGCGCAACTCGGCATCCAGAGCCCGCGGCA	180							
DB	196	CCACCATGAGCCTGCAATCTCAAGCCTCTGCGCAACTCGGCATCCAGAGCCCGCGGCA	255							
QY	181	CAGAGCACAGGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCTCTGCTGACCTTTGT	240							
DB	256	CAGAGCACAGGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCTCTGCTGACCTTTGT	315							
QY	241	GCTTGGTGTGCTGATAGGGCTGGCGCCCTGGGGCTTTGTTTTCAGTACTACACGC	300							
DB	316	GCTTGGTGTGCTGATAGGGCTGGCGCCCTGGGGCTTTGTTTTCAGTACTACACGC	375							
QY	301	TCTCCAATACTGGTCAAGACACCACTTCTCAATGGAGAAAGATTAGGAATACGTC	360							
DB	376	TCTCCAATACTGGTCAAGACACCACTTCTCAATGGAGAAAGATTAGGAATACGTC	435							
QY	361	AAGAGTGGCAATCTCTTCAAGTCCAGAAATATAAGCTTGCGAGAGTCTGCGAGCTGTGG	420							
DB	436	AAGAGTGGCAATCTCTTCAAGTCCAGAAATATAAGCTTGCGAGAGTCTGCGAGCTGTGG	495							
QY	421	CTGAAAACCTCTGCTGAGCTGTATACAAAGCTGGAGCACACAGGTGACGCTTGTGA	480							
DB	496	CTGAAAACCTCTGCTGAGCTGTATACAAAGCTGGAGCACACAGGTGACGCTTGTGA	555							
QY	481	CAGAAACAATGGAAATGGCATGGAGCAATTTGCTACAGTTCTATAAAGACAGCAAAAGTT	540							
DB	556	CAGAAACAATGGAAATGGCATGGAGCAATTTGCTACAGTTCTATAAAGACAGCAAAAGTT	615							
QY	541	GGGAGGACTGTAATATTTTCTGCTTGTAGTAAACCTCTACCATGTGAAGATAAACAAC	600							
DB	616	GGGAGGACTGTAATATTTTCTGCTTGTAGTAAACCTCTACCATGTGAAGATAAACAAC	675							
QY	601	AAGAAGACTGGAATTTGGCGCTCTCAGAGTACTCTGAGTTTCTACTCTTATTGGA	660							
DB	676	AAGAAGACTGGAATTTGGCGCTCTCAGAGTACTCTGAGTTTCTACTCTTATTGGA	735							
QY	661	CAGGCTCTTTTGGCGCTGACAGTGCAGAGGCTGGCTGGATGGATGGAACCCCTTTTCA	720							
DB	736	CAGGCTCTTTTGGCGCTGACAGTGCAGAGGCTGGCTGGATGGATGGAACCCCTTTTCA	795							
QY	721	CTTCTGAACTGTTCCATATTAATAGATGTCCAGAGCCCAAGAGACAGAGACTGTGTGG	780							
DB	796	CTTCTGAACTGTTCCATATTAATAGATGTCCAGAGCCCAAGAGACAGAGACTGTGTGG	855							
QY	781	CCATCTTAAATGGATGATCTTCTCAAGGACTGCAAGAAATGAAGCGTTGTCTGTG	840							
DB	856	CCATCTTCAATGGATGATCTTCTCAAGGACTGCAAGAAATGAAGCGTTGTCTGTG	915							
QY	841	ACAGAAGGCGCAGGAATGGTGAAGCGCAGAGAGCTCCATGTCCTCCCTGAAACATTAGGGG	900							
DB	916	ACAGAAGGCGCAGGAATGGTGAAGCGCAGAGAGCTCCATGTCCTCCCTGAAACATTAGGGG	975							

QY 901 AAGGTGACTGATTCCGCTCTGCAACTACAAATAGCAGAGTGAGCCAGCGGTGCAAG 960
KW |
KW |
DB 976 AAGGTGACTGATTCCGCTCTGCAACTACAAATAGCAGAGTGAGCCAGCGGTGCAAG 1035
QY 961 CAAGGGCTAGTTGAGACATTTGGAAATGGAACATAATCAGGAAAGACTATCTCTGACT 1020
DB 1036 CAAGGGCTAGTTGAGACATTTGGAAATGGAACATAATCAGGAAAGACTATCTCTGACT 1095
QY 1021 AGTACAAATGGTTCTCGTGTCTCTGTTTCTGAGGATCACAGCATTTCTGAGCTTGGTT 1080
DB 1096 AGTACAAATGGTTCTCGTGTCTCTGTTTCTGAGGATCACAGCATTTCTGAGCTTGGTT 1155
QY 1081 TATGACAGTATTTAAACAGTCAACAAGTCTTTATTTACATGCGCAACCAACCTCAGAA 1140
DB 1156 TATGACAGTATTTAAACAGTCAACAAGTCTTTATTTACATGCGCAACCAACCTCAGAA 1215
QY 1141 ACCCATATGTCATCTGCTCTTGGCTTAGAGATAAATTTTGTCTCTCTCTCA 1200
DB 1216 ACCCATATGTCATCTGCTCTTGGCTTAGAGATAAATTTTGTCTCTCTCTCA 1275
QY 1201 TGCTTAATATCACTCCCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTT 1260
DB 1276 TGCTTAATATCACTCCCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTT 1335
QY 1261 TTGAAGTAGAGGAAATACATTTGAGGTAAATCTTTCTGACAGTCAAGTAGTCCATC 1320
DB 1336 TTGAAGTAGAGGAAATACATTTGAGGTAAATCTTTCTGACAGTCAAGTAGTCCATC 1395
QY 1321 AGAAATTTGGCTGCTCTCCAGATTTGACCGCAAAATACAAAGAAATCTTTTGT 1380
DB 1396 AGAAATTTGGCTGCTCTCCAGATTTGACCGCAAAATACAAAGAAATCTTTTGT 1455
QY 1381 GTTTCAGTTCATCTAGTCCCTTCCCAATCCATCAGTAAAGACCCATCTGCTGTCCA 1440
DB 1456 GTTTCAGTTCATCTAGTCCCTTCCCAATCCATCAGTAAAGACCCATCTGCTGTCCA 1515
QY 1441 TGCCGTTTCCCAACAGGATGTCATCTGATATGAGAATCTCAATCTCAATGCCCTTATA 1500
DB 1516 TGCCGTTTCCCAACAGGATGTCATCTGATATGAGAATCTCAATCTCAATGCCCTTATA 1575
QY 1501 GCATTCCTCTGCTGCTCAATTAAGACTCTGATAATTTGTCTCCCTCCATAGAAATTTCTC 1560
DB 1576 GCATTCCTCTGCTGCTCAATTAAGACTCTGATAATTTGTCTCCCTCCATAGAAATTTCTC 1635
QY 1561 CCAGGAAAGAAATATATCCCATCTCCGTTTCATATCAGACTACCGTCCCGGATATCC 1620
DB 1636 CCAGGAAAGAAATATATCCCATCTCCGTTTCATATCAGAACTACCGTCCCGGATATTC 1695
QY 1621 CTTACAGAGATTAAGACCGAAAGAGTGAAGCTCTTCTATCTGCACTGTAAATAGTTT 1680
DB 1696 CTTACAGAGATTAAGACCGAAAGAGTGAAGCTCTTCTATCTGCACTGTAAATAGTTT 1755
QY 1681 CAGTTCCCTATTTCTTCCATTAAGACCGAAATTTATACCTTTGAGTCTGAAGATTTAATA 1740
DB 1756 CAGTTCCCTATTTCTTCCATTAAGACCGAAATTTATACCTTTGAGTCTGAAGATTTAATA 1815
QY 1741 ATAATAATGTAATACTGTGAATA 1766
DB 1816 ATAATAATGTAATACTGTGAATA 1841

RESULT 8

ID ABL95643 standard; cDNA; 1841 BP.

XX AC ABL95643;

XX AC ABL95643;

DT 19-JUL-2002 (first entry)

DE Human angiogenesis related cDNA PRO1131 SEQ ID NO: 165.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;

KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytosstatic; antiangiogenic; hypotensive; vulnerary;
XX antiarteriosclerotic; gene; ss.
OS Homo sapiens.
XX WO200208284-A2.
XX 31-JAN-2002.
XX 09-JUL-2001; 2001WO-US021735.
XX 20-JUL-2000; 2000US-0219558P.
XX 25-JUL-2000; 2000US-0220624P.
XX 25-JUL-2000; 2000US-0220664P.
XX 28-JUL-2000; 2000WO-US020710.
XX 02-AUG-2000; 2000US-0222695P.
XX 17-AUG-2000; 2000US-00643657.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
XX 07-SEP-2000; 2000US-0230978P.
XX 18-SEP-2000; 2000US-00664610.
XX 18-SEP-2000; 2000US-00665350.
XX 24-OCT-2000; 2000US-0242922P.
XX 08-NOV-2000; 2000US-00709238.
XX 08-NOV-2000; 2000WO-US030952.
XX 10-NOV-2000; 2000WO-US030873.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000US-00747259.
XX 20-DEC-2000; 2000WO-US034956.
XX 22-JAN-2001; 2001US-00767609.
XX 28-FEB-2001; 2001US-00796498.
XX 28-FEB-2001; 2001WO-US006520.
XX 01-MAR-2001; 2001WO-US006666.
XX 09-MAR-2001; 2001US-00802706.
XX 14-MAR-2001; 2001US-00808689.
XX 22-MAR-2001; 2001US-00816744.
XX 05-APR-2001; 2001US-00828366.
XX 10-MAY-2001; 2001US-00854208.
XX 10-MAY-2001; 2001US-00854280.
XX 25-MAY-2001; 2001US-00866028.
XX 25-MAY-2001; 2001US-00866034.
XX 30-MAY-2001; 2001WO-US017092.
XX 30-MAY-2001; 2001US-00870574.
XX 01-JUN-2001; 2001WO-US017443.
XX 20-JUN-2001; 2001WO-US017800.
XX 20-JUN-2001; 2001WO-US019692.
XX (GETH) GENENTECH INC.
XX (BAKE/) BAKER K P.
XX (FERR/) FERRARA N.
XX (GERB/) GERBER H.
XX (GERR/) GERRITSEN M E.
XX (GODD/) GODDARD A.
XX (GODO/) GODOWSKI P J.
XX (GURN/) GURNEY A L.
XX (HILL/) HILLAN K J.
XX (MARS/) MARSTERS S A.
XX (PANJ/) PAN J.
XX (PAON/) PAONI N F.
XX (STEP/) STEPHAN J F.
XX (WATA/) WATANABE C K.
XX (WILL/) WILLIAMS P M.
XX (WOOD/) WOOD W I.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2002-171999/22.

P-FSDB; ABE95505.

One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial PT infarction), endothelial or angiogenic disorders in a mammal.

Claim 1; Fig 165; 567pp; English.

The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention

Sequence 1841 BP: 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;

Query Match	99.3%;	Score 1764.4;	DB 6;	Length 1841;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1765;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0
Qy	1	AGCTCAGATGACCGCGCGCCAGGGCAATCCGACCAATTTCTACTCTCACCGCTGTAG	60	
Db	76	AGCTCAGATGACCGCGCGCCAGGGCAATCCGACCAATTTCTACTCTCACCGCTGTAG	135	
Qy	61	GAATCCAGATGACGCGCCAAAGTACAGCAGCACGAGGACATGCTGSGATGATGATGGGACA	120	
Db	136	GAATCCAGATGACGCGCCAAAGTACAGCAGCACGAGGACATGCTGSGATGATGATGGGACA	195	
Qy	121	CCACATGAGCGCTGGATTCTCAAGCCTTGCCCAACTCGGCATCCAGAGCCCCGGCGCA	180	
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XX 10-JUL-2003 (first entry)
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XX Human; PRO polypeptide; secreted protein; transmembrane protein;
KW chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast;
KW prostate; rectal; cervical; liver; cancer; TNF-alpha;
KW tumour necrosis factor-alpha; proliferation; differentiation;
KW chondrocyte cell; bone disorder; cartilage disorder; sports injury;
KW arthritis; cytostatic; antiarthritic; osteopathic; gene therapy; gene;
KW ss.
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OS Homo sapiens.
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Best Local Similarity 99.9%; Pred No. 0;
Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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XX	01-JUL-2003 (first entry)		
DT			
XX	Human secreted/transmembrane protein (PRO) cDNA #301.		
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XX	Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;		
KW	proliferation; differentiation; chondrocyte cells;		
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CC a method for detecting the presence of tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences cited
CC above. The PRO polypeptide or anti-PRO antibody is useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful
CC as hybridisation probes in chromosome and gene mapping, or in generating
CC anti-sense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
CC polypeptides, in assays to identify other proteins or molecules involved
CC in a binding reaction, to generate transgenic animals or knockout
CC animals, which in turn are useful in the development and screening of
CC therapeutically useful reagents, for chromosome identification, and
CC tissue typing. The PRO polypeptides and nucleic acid molecules are also
CC useful for detecting the presence of a tumour in a mammal, stimulating the
CC proliferation or differentiation of chondrocyte cells, stimulating the
CC release of tumour necrosis factor-alpha from human blood, in gene
CC therapy, or as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. The present sequence is a cDNA encoding a PRO
CC protein
XX

SQ Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;

Query Match 99.3%; Score 1764.4; DB 8; Length 1841;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 841 AGAGAAGGCGCAGGAATGTTGAAGCGCAGAGAGCTCCATGTCCCCCTGAAACATTAGGGG 900
DB 916 AGAGAAGGCGCAGGAATGTTGAAGCGCAGAGAGCTCCATGTCCCCCTGAAACATTAGGGG 975
QY 901 AAGTGAAGTGAATGCGCTCTGCAACTCAATAGCAGAGTGAAGCGGCTGCAAGAG 960
DB 976 AAGTGAAGTGAATGCGCTCTGCAACTCAATAGCAGAGTGAAGCGGCTGCAAGAG 1035
QY 961 CAAGGCTAGTTGAGACATTTGGGAATGGAACATAATCAGGAAGACTATCTCTGACT 1020
DB 1036 CAAGGCTAGTTGAGACATTTGGGAATGGAACATAATCAGGAAGACTATCTCTGACT 1095
QY 1021 AGTCAAAAATGGGTTCTCGTTTCTCTGTTTCTGAGTACCCAGCATTTCTGAGCTTGGGT 1080
DB 1096 AGTCAAAAATGGGTTCTCGTTTCTCTGTTTCTGAGTACCCAGCATTTCTGAGCTTGGGT 1155
QY 1081 TATGCACTGATTTAAACAGTCAAGAGAGTCTTATTTATGATGCAACCAACCTCAGAA 1140
DB 1156 TATGCACTGATTTAAACAGTCAAGAGAGTCTTATTTATGATGCAACCAACCTCAGAA 1215
QY 1141 ACCCATATGTCATCTGCTTCTTGGCTTAGAGATACTTTTAGCTCTCTTCTCTCAA 1200
DB 1216 ACCCATATGTCATCTGCTTCTTGGCTTAGAGATACTTTTAGCTCTCTTCTCTCAA 1275
QY 1201 TGTCTAAATACACCTCCCTGTTTCTGTTTCTTACACTTGGTGGAAATAGAAACTTT 1260
DB 1276 TGTCTAAATACACCTCCCTGTTTCTGTTTCTTACACTTGGTGGAAATAGAAACTTT 1335
QY 1261 TTGAAGTAGAGAAATATACATTGAGGTAAACATCTCTTCTGACAGTCAAGTGTGCTATC 1320
DB 1336 TTGAAGTAGAGAAATATACATTGAGGTAAACATCTCTTCTGACAGTCAAGTGTGCTATC 1395
QY 1321 AGAAATTGGCAGTCACTTCCAGATTTGACAGAAATATACCAAGAAATTTCTTTTGT 1380
DB 1396 AGAAATTGGCAGTCACTTCCAGATTTGACAGAAATATACCAAGAAATTTCTTTTGT 1455
QY 1381 GTTTCAGTTTCACTACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTGTCCA 1440
DB 1456 GTTTCAGTTTCACTACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTGTCCA 1515
QY 1441 TGCCGTTTCCCAAGGGATGTCACTTGTATGAGAACTCAAACTCAATGCTCAATGCTTATAA 1500
DB 1516 TGCCGTTTCCCAAGGGATGTCACTTGTATGAGAACTCAAACTCAATGCTCAATGCTTATAA 1575
QY 1501 GCATTCCTTCTGTTGCTCAATTAAGACTCTGATATTTGTTCTCCCTCCATAGGAATTTCTC 1560
DB 1576 GCATTCCTTCTGTTGCTCAATTAAGACTCTGATATTTGTTCTCCCTCCATAGGAATTTCTC 1635
QY 1561 CCAGAAAGAAATATATATCCCATCTCCGTTTCTCATAGAACTACCGTCCCGATATTTCC 1620
DB 1636 CCAGAAAGAAATATATATCCCATCTCCGTTTCTCATAGAACTACCGTCCCGATATTTCC 1695
QY 1621 CTTTCAGAGAGATTAAAGACCAAGAAAGAGTGAAGCTCTTCTATCTGCACCTGTAAATAGTT 1680
DB 1696 CTTTCAGAGAGATTAAAGACCAAGAAAGAGTGAAGCTCTTCTATCTGCACCTGTAAATAGTT 1755
QY 1681 CAGTTCCTTATTTTCTTCCATTTGACCCATATTTATACCTTTTTCAGTACTGGAAGATTATA 1740
DB 1756 CAGTTCCTTATTTTCTTCCATTTGACCCATATTTATACCTTTTTCAGTACTGGAAGATTATA 1815
QY 1741 ATATAAATGTAAATACTGTGAAAAA 1766
DB 1816 ATATAAATGTAAATACTGTGAAAAA 1841

QY 241 GCTTGGTGTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTCTTTTTCAGTACTACCAGC 300
Db 316 GCTTGGTGTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTCTTTTTCAGTACTACCAGC 375
QY 301 TCTCCAAATCTGGTCAAGACACCATTTCTCAAAATGGAAGAAAGATTAGGAAATACGTCCC 360
Db 376 TCTCCAAATCTGGTCAAGACACCATTTCTCAAAATGGAAGAAAGATTAGGAAATACGTCCC 435
QY 361 AAGAGTTGCAATCTCTTTCAAGTCCAGAAATATAAAGCTTCGAGAAAGTCTGACAGATGCG 420
Db 436 AAGAGTTGCAATCTCTTTCAAGTCCAGAAATATAAAGCTTCGAGAAAGTCTGACAGATGCG 495
QY 421 CTGAAAACTCTGCTGGAGCTGTATACAAAGCTGGAGCACACAGGTGACGCCCTTGTGA 480
Db 496 CTGAAAACTCTGCTGGAGCTGTATACAAAGCTGGAGCACACAGGTGACGCCCTTGTGA 555
QY 481 CAGAACATGGAATGGCATGGAGCAATTTGCTACCAAGTCTTATAAAGACAGCAAAAGTT 540
Db 556 CAGAACATGGAATGGCATGGAGCAATTTGCTACCAAGTCTTATAAAGACAGCAAAAGTT 615
QY 541 GGGAGGACTGTAATAATTTTCCCTTAGTGAAGAACTCTACCATGCTGGAAGATAAACAAC 600
Db 616 GGGAGGACTGTAATAATTTTCCCTTAGTGAAGAACTCTACCATGCTGGAAGATAAACAAC 675
QY 601 AAGAAGACCTGGAATTTGGCCGCTCTCAGAGCTACTCTCAGTCTTCTTACTCTTATTGGA 660
Db 676 AAGAAGACCTGGAATTTGGCCGCTCTCAGAGCTACTCTCAGTCTTCTTACTCTTATTGGA 735
QY 661 CAGGGCTTTTGGCCCTGACAGTGGCAAGCCCTGGCTGGATGGATGGAACCCCTTTTCA 720
Db 736 CAGGGCTTTTGGCCCTGACAGTGGCAAGCCCTGGCTGGATGGATGGAACCCCTTTTCA 795
QY 721 CTTCTGAACCTGTTCCATATTATAATAGATGTCAACAGCCCAAGAGCAGAGACTGTGTGG 780
Db 796 CTTCTGAACCTGTTCCATATTATAATAGATGTCAACAGCCCAAGAGCAGAGACTGTGTGG 855
QY 781 CCATCTTAAATGGATGATCTCTCAGAGCTGCAAGAGCTGCAAGAAATGAAGCGTTGTGTGG 840
Db 856 CCATCTTAAATGGATGATCTCTCAGAGCTGCAAGAGCTGCAAGAAATGAAGCGTTGTGTGG 915
QY 841 ACAGAGGCGCAGGAATGGTGAAGCCAGAGAGCTCCATGTCCTCCCTGAAACATTAGGCG 900
Db 916 ACAGAGGCGCAGGAATGGTGAAGCCAGAGAGCTCCATGTCCTCCCTGAAACATTAGGCG 975
QY 901 AAGGTGACTGATTGCGCCCTCTGCAACTCAAAATAGCAGAGTGAAGCCGCGTGCACAAAG 960
Db 976 AAGGTGACTGATTGCGCCCTCTGCAACTCAAAATAGCAGAGTGAAGCCGCGTGCACAAAG 1035
QY 961 CAAGGGCTAGTTGAGACATGGGAATGGAACATATCAGGAAAGACTATCTCTGACT 1020
Db 1036 CAAGGGCTAGTTGAGACATGGGAATGGAACATATCAGGAAAGACTATCTCTGACT 1095
QY 1021 AGTACAAAATGGTTCCTGCTGTTCTCTGTTCCAGGATCACAGCATTTCTGAGCTTGGTT 1080
Db 1096 AGTACAAAATGGTTCCTGCTGTTCTCTGTTCCAGGATCACAGCATTTCTGAGCTTGGTT 1155
QY 1081 TATGCAAGTATTAAACAGTCAAGAAGTCTTATTATGATGCCAACCAACCTCAGAA 1140
Db 1156 TATGCAAGTATTAAACAGTCAAGAAGTCTTATTATGATGCCAACCAACCTCAGAA 1215
QY 1141 ACCCATATATGCTATGCTGCTTGGCTTAGAGATAAATTTTAGCTCTCTTTCTCTCAA 1200
Db 1216 ACCCATATATGCTATGCTGCTTGGCTTAGAGATAAATTTTAGCTCTCTTTCTCTCAA 1275
QY 1201 TGTCTAATATCACTCCCTGTTTTCATGCTCTTCTCTTACACTTGGTGAATAGAACTTT 1260
Db 1276 TGTCTAATATCACTCCCTGTTTTCATGCTCTTCTCTTACACTTGGTGAATAGAACTTT 1335
QY 1261 TTGCAAGTAGAGGAAATACATTGAGGTAAACATCTTTCTCTGACAGTCAAGTAGTCCATC 1320
Db 1336 TTGCAAGTAGAGGAAATACATTGAGGTAAACATCTTTCTCTGACAGTCAAGTAGTCCATC 1395

QY 1321 AGAAATGGCAGTCACTTCCAGATTGTACCCAGCAAAATACACAAGAAATTTCTTTTGT 1380
Db 1396 AGAAATGGCAGTCACTTCCAGATTGTACCCAGCAAAATACACAAGAAATTTCTTTTGT 1455
QY 1381 GTTTCAGTTCATACCTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTGTCCA 1440
Db 1456 GTTTCAGTTCATACCTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTGTCCA 1515
QY 1441 TGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAAATCTCAATCTCAATGCTTATAA 1500
Db 1516 TGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAAATCTCAATCTCAATGCTTATAA 1575
QY 1501 GCATTCCTTCTGCTGCTCCATTAAGACTCTGATAATTTGTCTCCCTCCATAGGAATTTCTC 1560
Db 1576 GCATTCCTTCTGCTGCTCCATTAAGACTCTGATAATTTGTCTCCCTCCATAGGAATTTCTC 1635
QY 1561 CCAGGAAAGAAATATATCCCATCTCCGTTTTCATATCAGAACTACCGTCCCGATATTC 1620
Db 1636 CCAGGAAAGAAATATATCCCATCTCCGTTTTCATATCAGAACTACCGTCCCGATATTC 1695
QY 1621 CTTTCAGAGAGATTAAAGACCAAGAAAGTGAAGCTCTTTCATCTGCACTGCACTGTAATAGTTT 1680
Db 1696 CTTTCAGAGAGATTAAAGACCAAGAAAGTGAAGCTCTTTCATCTGCACTGTAATAGTTT 1755
QY 1681 CAGTTTCTTATTTTCTTCCATTTGACCCATATTTATACCTTTTCAGGTACTGCAAGATTTAATA 1740
Db 1756 CAGTTTCTTATTTTCTTCCATTTGACCCATATTTATACCTTTTCAGGTACTGCAAGATTTAATA 1815
QY 1741 ATAATAAATGTAATACTGTGAAAAA 1766
Db 1816 ATAATAAATGTAATACTGTGAAAAA 1841
RESULT 12
ACA66834
ID ACA66834 standard; cDNA; 1841 BP.
XX ACA66834;
XX 23-JUN-2003 (first entry)
XX cDNA encoding human PRO protein #301.
XX Human; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;
XX Liver; PRO; gene therapy; gene; ss.
XX Homo sapiens.
XX US2003036137-A1.
XX 20-FEB-2003.
XX 27-JUN-2002; 2002US-00184640.
XX 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 18-OCT-1999; 99US-00403297.

PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028551.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUN-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021086.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001WO-US027099.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-00052586.

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL,
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-342038/32.
P-PSDB; AB080734.

Three hundred and five nucleic acids encoding secreted and transmembrane
PRO polypeptides, useful for the diagnosis, prevention and/or treatment
of tumors, such as adrenal, lung, colon, breast, prostate, rectal,
cervical or liver tumors.

Claim 2; Fig 601; 708pp; English.

The invention relates to three hundred and five nucleic acids encoding
PRO polypeptides (secreted and transmembrane). Methods and compositions
of the present invention are useful for the diagnosis, prevention and/or
treatment of tumors, such as adrenal, lung, colon, breast, prostate,
rectal, cervical or liver tumors. The PRO polypeptides are also useful
as molecular weight markers, or for chromosome identification. The PRO
genes are useful as hybridisation probes, or for screening libraries of
human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
therapy, particularly for replacing a defective gene. The present
sequence represents a cDNA encoding a human PRO polypeptide of the
invention

XX Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;
SQ
Query Match
Best Local Similarity 99.3%; Score 1764.4; DB 8; Length 1841;
Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGCTCACAGTAGCCCGCGCCAGGGCAATCCGACCAATTTCACCTCACCGCTGTAG 60
DB 76 AGCTCACAGTAGCCCGCGCCAGGGCAATCCGACCAATTTCACCTCACCGCTGTAG 135
QY 61 GAATCCAGATCCAGGCCCAAGTACAGCAGCAGAGGACATCTGGATGATATGGGGACA 120
DB 136 GAATCCAGATCCAGGCCCAAGTACAGCAGCAGAGGACATCTGGATGATATGGGGACA 195
QY 121 CCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCGGGCGCA 180
DB 196 CCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCGGGCGCA 255
QY 181 CAGAGCACAGGGCTCCCTCTTTCAACGTGGCGACAGTGGCCCTGACCTGTGACTTTGT 240
DB 256 CAGAGCACAGGGCTCCCTCTTTCAACGTGGCGACAGTGGCCCTGACCTGTGACTTTGT 315
QY 241 GCTTGGTCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTCTTTTTCAGTACTACACAGC 300
DB 316 GCTTGGTCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTCTTTTTCAGTACTACACAGC 375
QY 301 TCTCCAATACGTGTCACAGACACCAATTTCTCAATGGAAGAAAGATTAGGAAATACGTCCC 360
DB 376 TCTCCAATACGTGTCACAGACACCAATTTCTCAATGGAAGAAAGATTAGGAAATACGTCCC 435
QY 361 AAGAGTTGCAATCTCTTCAAGTCCAGAAATATAAGCTTTCAGGAAAGTCTGAGCATGTGG 420
DB 436 AAGAGTTGCAATCTCTTCAAGTCCAGAAATATAAGCTTTCAGGAAAGTCTGAGCATGTGG 495
QY 421 CTGAAAAACTCTGCTGAGCTGTATACAAAGCTGGAGCACACAGTGGCAGCCCTTCTGA 480
DB 496 CTGAAAAACTCTGCTGAGCTGTATACAAAGCTGGAGCACACAGTGGCAGCCCTTCTGA 555
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DB 556 CAGAACTGGAATGCGATCGAGACAAATTCGTACCAAGTCTTATAAAGACAGCAAAAGTT 615
QY 541 GGGAGGACTGTAAATATTTTCTGCCTTAGTGAAGAACTCTACCATGCTGAAGATAAACAAAC 600
DB 616 GGGAGGACTGTAAATATTTTCTGCCTTAGTGAAGAACTCTACCATGCTGAAGATAAACAAAC 675
QY 601 AAGAAGACTGGAATTTGCGCGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGA 660
DB 676 AAGAAGACTGGAATTTGCGCGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGA 735
QY 661 CAGGCTTTTTCGCGCTCTCAGAGCTGCAAGGCTTGGCTGTGATGGATGGAACCCCTTTCA 720
DB 736 CAGGCTTTTTCGCGCTCTCAGAGCTGCAAGGCTTGGCTGTGATGGATGGAACCCCTTTCA 795
QY 721 CTTCTGAACTGTTCATATTAATAGATGTACACAGCCCAAGAGCAGAGACTGTGTGG 780
DB 796 CTTCTGAACTGTTCATATTAATAGATGTACACAGCCCAAGAGCAGAGACTGTGTGG 855
QY 781 CCATCTTAAATGGGATGATCTTCTCAAGGAGCTGCAAGAAATTTGAAGCGTTGTGTCTGTG 840
DB 856 CCATCTCTCAATGGGATGATCTTCTCAAGGAGCTGCAAGAAATTTGAAGCGTTGTGTCTGTG 915
QY 841 AGAGAAGGCGCAGGAATGTTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTTAGGCG 900
DB 916 AGAGAAGGCGCAGGAATGTTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTTAGGCG 975
QY 901 AAGGTGACTGATTGCGCCCTCTGCAACTACAATAGCAGAGTGAAGCCGCGTGCAGAG 960
DB 976 AAGGTGACTGATTGCGCCCTCTGCAACTACAATAGCAGAGTGAAGCCGCGTGCAGAG 1035
QY 961 CAAGGGCTAGTTGAGACATTTGGGAATGGAACATTAATCAGGAAGACTATCTCTGTACT 1020

Db	1036	CAAGGCTAGTTGAGACATTGGGAATGGAAATATATCAGGAAGACTATCTCTCTGACT	1095	XX	US2003003531-A1.
Qy	1021	AGTACAAATGGGTTCTCGTGTCTCTGTTTACAGGATCAGCAGATTTCTGAGCTTGGGTT	1080	XX	02-JAN-2003.
Db	1096	AGTACAAATGGGTTCTCGTGTCTCTGTTTACAGGATCAGCAGATTTCTGAGCTTGGGTT	1155	XX	19-NOV-2001; 2001US-00989734.
Qy	1081	TATGACAGTATTTAAACAGTACAGGATCTTATTTACATGACCAACCAACCTCAGAA	1140	XX	16-JUN-1997; 97US-0049787P.
Db	1156	TATGACAGTATTTAAACAGTACAGGATCTTATTTACATGACCAACCAACCTCAGAA	1215	XX	17-OCT-1997; 97US-0062250P.
Qy	1141	ACCCATAATGTCTATTCGCTTCTTGGCTTACAGATTAACCTTTTAGCTCTCTTCTCTCAA	1200	XX	05-NOV-1997; 97WO-US020069.
Db	1216	ACCCATAATGTCTATTCGCTTCTTGGCTTACAGATTAACCTTTTAGCTCTCTTCTCAA	1275	XX	12-NOV-1997; 97US-0065186P.
Qy	1201	TGTCTAATATCATCTCCCTCGTTTTCATGCTCTTCTTCTTCACTTGGTGGATTAAGAACTTT	1260	XX	13-NOV-1997; 97US-0065311P.
Db	1276	TGTCTAATATCATCTCCCTCGTTTTCATGCTCTTCTTCTTCACTTGGTGGATTAAGAACTTT	1335	XX	24-NOV-1997; 97US-0066770P.
Qy	1261	TTGAAGTAGAGGAATACATTCAGGTAACTCTTCTCTGACAGTCAAGTAGTCCATC	1320	XX	25-FEB-1998; 98US-0075945P.
Db	1336	TTGAAGTAGAGGAATACATTCAGGTAACTCTTCTCTGACAGTCAAGTAGTCCATC	1395	XX	20-MAR-1998; 98US-0078910P.
Qy	1321	AGAAATTTGGCAGTCACTTCCAGATTTGACAGCAAAATACACAAAGAAATCTTTTGT	1380	XX	28-APR-1998; 98US-0083322P.
Db	1396	AGAAATTTGGCAGTCACTTCCAGATTTGACAGCAAAATACACAAAGAAATCTTTTGT	1455	XX	07-MAY-1998; 98US-0084600P.
Qy	1381	GTTTCAGTTTCATAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTGTCCA	1440	XX	28-MAY-1998; 98US-0087106P.
Db	1456	GTTTCAGTTTCATAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTGTCCA	1515	XX	02-JUN-1998; 98US-0087607P.
Qy	1441	TGCGGTTTCCCAACAGGATGTCATTTGATATGAGATCTCAATCTCAATGCTTATAA	1500	XX	02-JUN-1998; 98US-0087609P.
Db	1516	TGCGGTTTCCCAACAGGATGTCATTTGATATGAGATCTCAATCTCAATGCTTATAA	1575	XX	03-JUN-1998; 98US-0087759P.
Qy	1501	GCAATTCCTTCTGTTGCAATTAAGACTCTGATAATTTGCTCCCTCCATAGGAATTTCTC	1560	XX	04-JUN-1998; 98US-0088021P.
Db	1576	GCAATTCCTTCTGTTGCAATTAAGACTCTGATAATTTGCTCCCTCCATAGGAATTTCTC	1635	XX	04-JUN-1998; 98US-0088025P.
Qy	1561	CCAGAAAGAAAT	1620	XX	04-JUN-1998; 98US-0088026P.
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Qy	1621	CTTCAGAGATTAAGACCAAGAAAGTGGAGCTCTTCATCTGCCTGTGAATAGTTT	1680	XX	05-JUN-1998; 98US-0088167P.
Db	1696	CTTCAGAGATTAAGACCAAGAAAGTGGAGCTCTTCATCTGCCTGTGAATAGTTT	1755	XX	05-JUN-1998; 98US-0088202P.
Qy	1681	CAGTTCTCTATTTCTTCCATTCACCATATATATATATATATATATATATATATAT	1740	XX	05-JUN-1998; 98US-0088212P.
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Qy	1741	ATAATAAATGTAATACTGTGAAAAA	1766	XX	10-JUN-1998; 98US-008834P.
Db	1816	ATAATAAATGTAATACTGTGAAAAA	1841	XX	10-JUN-1998; 98US-0088734P.
RESULT 13					
ACAG4371					
ID	ACAG4371	standard; cdna; 1841 BP.			
XX	ACAG4371;				
AC	ACAG4371;				
XX	ACAG4371;				
DT	17-JUN-2003	(first entry)			
XX	ACAG4371;				
DE	Novel human secreted and transmembrane protein PRO1131	cdna.			
KW	Human; secreted and transmembrane protein; cytostatic; anti-HIV;				
KW	virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;				
KW	PRO; pharmaceutical; diagnostic; biosensor; bioindicator; malignancy;				
KW	cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;				
KW	lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;				
XX	drug screening; gene; ss.				
XX	Homo sapiens.				
OS					

```
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001WO-US021992.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Klijavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-352829/33.
XX P-PSDB; ABU72542.
XX
XX New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
PT disease.
XX
PS Claim 1; Fig 229; 663pp; English.
XX
XX The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
CC are particularly useful for detecting or treating e.g. malignancies or
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
CC leukemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's
CC disease in mammals. The PRO polypeptides are useful in drug screening,
CC particularly as targets for therapeutic intervention in these diseases,
CC and in the diagnostic determination of the presence of these diseases.
CC The PRO polypeptides are also useful as molecular weight markers, or for
CC chromosome identification. The PRO genes are useful as hybridisation
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC The PRO genes may also be used in gene therapy, particularly for
CC replacing a defective gene. This sequence encodes a novel human secreted
CC and transmembrane PRO polypeptide
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Query Match 99.3%; Score 1764.4; DB 8; Length 1841;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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XX KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX KW chondrocyte; proliferation; differentiation; cartilage disorder;
XX KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
XX KW liver; drug screening; transgenic animal; genetic analysis;
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XX OS Homo sapiens.
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XX PD 27-FEB-2003.
XX PF 26-JUN-2002; 2002US-00183006.
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KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 17:30:12 ; Search time 7523 Seconds
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11439.115 Million cell updates/sec

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Searched: 4708233 seqs, 24227607955 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1
BD074859
LOCUS
DEFINITION Secreted proteins and polynucleotide encoding the same.
ACCESSION BD074859
VERSION BD074859.1 GI:22620462
KEYWORDS JP 2001515717-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1776)
AUTHORS Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Evans,C.,
Merberg,D., Treacy,M., Agostino,M.J. and Spaulding,V.
TITLE Secreted proteins and polynucleotide encoding the same
JOURNAL Patent: JP 2001515717-A 1 25-SEP-2001;
GENETICS INSTITUTE INC
COMMENT OS Homo sapiens (human)
PN JP 2001515717-A/1
PD 25-SEP-2001
PF 08-SEP-1997 US 08/929007
PI KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI
PI CHERYL EVANS,
PI DAVID MERBERG,MAURICE TREACY,MICHAEL J AGOSTINO,VIKKI PI
SPAUDLING
PC C12N15/09,A61K38/00,A61P43/00,C07K14/52,C12N1/21, PC
C12N5/10,
PC C12N15/00,A61K37/02,A61K37/18,C12N5/00
CC Secreted proteins and polynucleotide encoding the same FH
Key Location/Qualifiers
FT source 1..1776
FT /organism='Homo sapiens (human)'.
FEATURES
source
Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 1776; DB 6; Length 1776;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTCAGTAGCCCGCGCGCCAGGGCAATCGGACCAATTTCACTCTCACCGCTGTAG 60
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QY 61 GAATCCAGATGACGGCCAAAGTACAGCAGCAGCAGGACATGCTGGATGATGAGGGACA 120
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DB 1816 ATAAATAATGTAATACTGTGAAAAA 1841

RESULT 3

AR528680
LOCUS AR528680 1841 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 457 from patent US 6725730.
ACCESSION AR528680
VERSION AR528680.1 GI:53916758
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1841)
AUTHORS Bollinger, C.L., Jr.
TITLE Crane test weight assembly and method
JOURNAL Patent: US 6725730-A 457 27-APR-2004;
FEATURES
Location/Qualifiers
1..1841
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 99.3%; Score 1764.4; DB 6; Length 1841;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTCAGTAGCCCGGCGGCCAGGGCAATCCGACCAATTTCACTCTCACCGCTGTAG 60
Db 76 AGCTCAGTAGCCCGGCGGCCAGGGCAATCCGACCAATTTCACTCTCACCGCTGTAG 135
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QY 181 CAGAGCACAGGCTCCCTCTTCAAGCTGGCGACAGTGGCCCTGACCCCTGCTGACTTGT 240
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RESULT 4

AX055702

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1

Baker, K.P.,

Goddard, A.,

Gurney, A.L.,

Hebert, C.,

Henzel, W.,

Kabakoff, R.C.,

Shelton, D.L.,

Smith, V.,

Watanabe, C.K.,

and Wood, W.I.

Methods and

compositions

for inhibiting

neoplastic cell growth

Patent: WO 0073348-A 17 07-DEC-2000;

Genentech, Inc. (US)

Location/Qualifiers

1. .1841

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Sequence 17 from Patent WO0073348.

AX055702.1 GI:12228834

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.

Baker, K.P.,

Goddard, A.,

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Kabakoff, R.C.,

Shelton, D.L.,

Smith, V.,

Watanabe, C.K.,

and Wood, W.I.

Methods and

compositions

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neoplastic cell growth

Patent: WO 0073348-A 17 07-DEC-2000;

Genentech, Inc. (US)

Location/Qualifiers

1. .1841

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 99.3%; Score 1764.4; DB 6; Length 1841;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTCACAGTAGCCCGCGCCAGGCAATCCGACCAATTTCACTCTCACCGTGTAG 60
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RESULT 5

LOCUS AX376534 1841 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 601 from Patent WO0168848.
ACCESSION AX376534
VERSION AX376534.1 GI:19170655
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 601 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
Location/Qualifiers
1..1841

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

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Query Match          99.3%; Score 1764.4; DB 6; Length 1841;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 6

AX403431
LOCUS AX403431
DEFINITION Sequence 318 from Patent WO0073454.
ACCESSION AX403431
VERSION AX403431.1
KEYWORDS GI:21436942

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS

Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnovers, L., Eaton, D.,
Ferrara, N., Gerber, H., Gertsen, M., Goddard, A., Godowski, P.,
Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J.,
Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,

TITLE Williams, P., Wood, W.I. and Zhang, Z.									
Secreted and transmembrane polypeptides and nucleic acids encoding the same									
JOURNAL Patent: WO 0073454-A 318 07-DEC-2000;									
Genentech Inc. (US)									
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Query Match 99.3%; Score 1764.4; DB 6; Length 1841;									
Best Local Similarity 99.9%; Pred. No. 0;									
Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
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RESULT 7
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LOCUS AX454580
DEFINITION Sequence 165 from Patent WO0208284.
ACCESSION AX454580
VERSION AX454580.1 GI:21713914
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

linear DNA 1841 bp PAT 06-JUL-2002

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.P., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.

Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0208284-A 165 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)

Location/Qualifiers
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Query Match 99.3%; Score 1764.4; DB 6; Length 1841;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTCACAGTACCGCGGGCCAGGCAATCCGACCACTTCACTCTCACCGCTGTAG 60
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RESULT 8
AX464324
LOCUS AX464324 1841 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 457 from Patent WO0140466.
ACCESSION AX464324
VERSION AX464324.1 GI:21899178
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.L. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 457 07-JUN-2001;
Genentech Inc. (US)
FEATURES
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LOCUS
DEFINITION Sequence 165 from Patent WO0200690.
ACCESSION AX491058
VERSION AX491058.1 GI:22323866
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0200690-A 165 03-JAN-2002;
Genentech, Inc. (US)
FEATURES
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/mol_type="unassigned DNA"
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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LOCUS Homo sapiens clone DNA59777 QAKY569 (UNQ569) mRNA PRI 03-OCT-2003
ACCESSION AY358587
VERSION AY358587.1 GI:37182295
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1841)

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Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,
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Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
Goddard, A., Wood, W.I. and Godowski, P.

TITLE

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment

Genome Res. 13 (10), 2265-2270 (2003)

12975309

JOURNAL

PUBLISHED

REFERENCE

AUTHORS

TITLE

JOURNAL

Inc., 1 DNA Way, South San Francisco, CA 94080, USA

Location/Qualifiers

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Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION Homo sapiens C-type lectin-like receptor-1, mRNA (cdna clone
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ACCESSION BC067746
VERSION BC067746.1 GI:45709962

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 2701)

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Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 2701)

Strausberg, R.

Direct Submission

Submitted (19-MAR-2004) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

cDNA Library Preparation: Michael Brownstein / Ted Usdin

Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www.shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: TRAK Plate: 168 Row: k Column: 9

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 23503320.

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LOCUS	Primer for synthesizing full-length cDNA and use thereof.			
DEFINITION	BD127503			
ACCESSION	BD127503.1	GI:23222448		
VERSION	JP 2002017375-A/2934			
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 1756)			

AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayaashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,I. and
Koga,H.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002017375-A/2934
PD 22-JAN-2002 JP 2002053172
PF 07-JUL-2000 JP 2002053172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
PI ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NACAI, PI
SHINICHI KOJIMA,
PI TETSUO OTSUKI, HISASHI KOGA
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10,
PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
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FT CDS
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1756; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 14
AK075114
LOCUS AK075114 1756 bp mRNA linear PRI 03-SEP-2002
DEFINITION Homo sapiens cDNA FLJ90633 fis, clone PLACE1003573, weakly similar
to T-CELL SURFACE GLYCOPROTEIN YEI/48.

ACCESSION AK075114
VERSION AK075114.1 GI:22760991
KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T.,
Sugiyama, T., Suzuki, Y., Negai, K., Sugano, S., Ishii, S.,
Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y.,
Kojima, S., Nagahara, K., Maezumi, Y., Ono, T., Okano, K., Yoshikawa, Y.,
Aotseuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and
Ninomiya, K.

TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1756)
AUTHORS Isogai, T. and Otsuki, T.

TITLE Direct Submission
JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).

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ORIGIN
Query Match 98.9%; Score 1756; DB 9; Length 1756;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1756; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACAGTAGCCCGCGCCAGGCAATTCGACCACATTTTCACTCTCACCGCTGTAGGAATC 65
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RESULT 15

BC039072

LOCUS

DEFINITION Homo sapiens C-type lectin-like receptor-1, mRNA (cDNA clone

MGC:34328 IMAGE:5178017), complete cds.

ACCESSION BC039072

VERSION BC039072.1 GI:24660225

KEYWORDS MGC.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1797)

Authors Klausner, R.D., Collins, F.S., Wagner, L., Shemen, C.M., Schuler, G.D.,

Altshuler, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carrinci, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abrahamson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahy, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shvchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, O., Smailus, D.E.,

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932

2 (bases 1 to 1797)

Strausberg, R.

Direct Submission

Submitted (01-NOV-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louie, H.,

Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,

A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 51 Row: 0 Column: 12

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 7706062.

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GEED"

ORIGIN

Query Match

Best Local Similarity

Matches 1756; Conservative

98.8%; Score 1755.4; DB 9; Length 1797;

99.9%; Pred. No. 0;

Mismatches 1; Indels 0; Gaps 0;

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Db 1 GCCCAGGGCAATCCGACCATTTTCTCTCAGCTAGGATCCAGATCCAGCCAA 60

Qy 80 GTACAGCAGCAGGAGGACATCTCGATGATGAGGACACCCACCATGAGCTCATTC 139

Db 61 GTACAGACGACGAGGACATCTCGATGATGATGGGACACCAACATGAGCCTCATTC 120
Qy 140 TCAAGCCTCTGCAACAACCTCGCATCTCAGAGCCCGGCGCACAGAGCACAGGGCTCCCTC 199
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Qy 1100 CACAAGAAGTCTTATTTATGATGCCCAACCAACCTCAGAAACCCATATGTCTGCTGCC 1159
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GenCore version 5.1.6
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ALIGNMENTS

RESULT 1
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; Sequence 2, Application US/09055095
; Patent No. 5945308
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Patterson, Chandra
; APPLICANT: Corley, Neil C.
; APPLICANT: Sather, Susan
; TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/055,095
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0500 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGN0T09
; CLONE: 1355922
US-09-055-095-2

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RESULT 2

US-09-643-597-194
; Sequence 194, Application US/09643597
; Patent No. 6426072

GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 194
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-643-597-194

Query Match 18.0%; Score 320; DB 3; Length 320;
Best Local Similarity 100.0%; Pred. No. 3.9e-90;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1399 CCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTGTCATGCGTTTCCCAACAGGG 1458
Db 1 CCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTGTCATGCGTTTCCCAACAGGG 60

QY 1459 ATGTCACTTGATGAGAACTCAAAATCTCAATGCTTATAAGCAATCTCTCTGTGTCC 1518
Db 61 ATGTCACTTGATGAGAACTCAAAATCTCAATGCTTATAAGCAATCTCTCTGTGTCC 120

QY 1519 ATTAAGACTCTGATAATTTGCTCTCCCTCCATAGGAATTTCTCCAGGAAGAAATATATC 1578
Db 121 ATTAAGACTCTGATAATTTGCTCTCCCTCCATAGGAATTTCTCCAGGAAGAAATATATC 180

QY 1579 CCATCTCCGTTTCATATCAGAACTACCGTCCCGATATTCCTTTCAGAGAGATTAAAGA 1638
Db 181 CCATCTCCGTTTCATATCAGAACTACCGTCCCGATATTCCTTTCAGAGAGATTAAAGA 240

QY 1639 CCAGAAAAAGTGAGCTCTTCATCTGCACCTGTAATAGTTTCAGTTCTCTTTCTTCC 1698
Db 241 CCAGAAAAAGTGAGCTCTTCATCTGCACCTGTAATAGTTTCAGTTCTCTTTCTTCC 300

QY 1699 ATTGACCCATATTATACCT 1718
Db 301 ATTGACCCATATTATACCT 320

RESULT 3

US-09-480-884A-194
; Sequence 194, Application US/09480884A
; Patent No. 6482597

GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Hosken, Nancy A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

; FILE REFERENCE: 210121.455C6

; CURRENT APPLICATION NUMBER: US/09/480,884A

; CURRENT FILING DATE: 2001-08-27

; NUMBER OF SEQ ID NOS: 330

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 194

; LENGTH: 320

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-480-884A-194

Query Match 18.0%; Score 320; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 3.9e-90;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1399 CCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTGTCATGCGTTTCCCAACAGGG 1458
Db 1 CCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTGTCATGCGTTTCCCAACAGGG 60

QY 1459 ATGTCACTTGATGAGAACTCAAAATCTCAATGCTTATAAGCAATCTCTCTGTGTCC 1518
Db 61 ATGTCACTTGATGAGAACTCAAAATCTCAATGCTTATAAGCAATCTCTCTGTGTCC 120

QY 1519 ATTAAGACTCTGATAATTTGCTCTCCCTCCATAGGAATTTCTCCAGGAAGAAATATATC 1578
Db 121 ATTAAGACTCTGATAATTTGCTCTCCCTCCATAGGAATTTCTCCAGGAAGAAATATATC 180

QY 1579 CCATCTCCGTTTCATATCAGAACTACCGTCCCGATATTCCTTTCAGAGAGATTAAAGA 1638
Db 181 CCATCTCCGTTTCATATCAGAACTACCGTCCCGATATTCCTTTCAGAGAGATTAAAGA 240

QY 1639 CCAGAAAAAGTGAGCTCTTCATCTGCACCTGTAATAGTTTCAGTTCTCTTTCTTCC 1698
Db 241 CCAGAAAAAGTGAGCTCTTCATCTGCACCTGTAATAGTTTCAGTTCTCTTTCTTCC 300

QY 1699 ATTGACCCATATTATACCT 1718
Db 301 ATTGACCCATATTATACCT 320

RESULT 4

US-09-542-615A-194
; Sequence 194, Application US/09542615A
; Patent No. 6518256

GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy A.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

; FILE REFERENCE: 210121.455C8

; CURRENT APPLICATION NUMBER: US/09/542,615A

; CURRENT FILING DATE: 2000-04-14

; NUMBER OF SEQ ID NOS: 350

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 194

; LENGTH: 320

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-542-615A-194

Query Match 18.0%; Score 320; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 3.9e-90;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1399 CCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTGTCATGCGTTTCCCAACAGGG 1458
Db 1 CCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTGTCATGCGTTTCCCAACAGGG 60

QY 1459 ATGTCACTTGATGAGAACTCAAAATCTCAATGCTTATAAGCAATCTCTCTGTGTCC 1518
Db 61 ATGTCACTTGATGAGAACTCAAAATCTCAATGCTTATAAGCAATCTCTCTGTGTCC 120

QY 1519 ATTAAGACTCTGATAATTTGCTCTCCCTCCATAGGAATTTCTCCAGGAAGAAATATATC 1578
Db 121 ATTAAGACTCTGATAATTTGCTCTCCCTCCATAGGAATTTCTCCAGGAAGAAATATATC 180

QY 1579 CCATCTCCGTTTCATATCAGAACTACCGTCCCGATATTCCTTTCAGAGAGATTAAAGA 1638
Db 181 CCATCTCCGTTTCATATCAGAACTACCGTCCCGATATTCCTTTCAGAGAGATTAAAGA 240

QY 1639 CCAGAAAAAGTGAGCTCTTCATCTGCACCTGTAATAGTTTCAGTTCTCTTTCTTCC 1698
Db 241 CCAGAAAAAGTGAGCTCTTCATCTGCACCTGTAATAGTTTCAGTTCTCTTTCTTCC 300

QY 1699 ATTGACCCATATTATACCT 1718
Db 301 ATTGACCCATATTATACCT 320

RESULT 5

US-09-606-421B-194
; Sequence 194, Application US/09606421B
; Patent No. 6531315

GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 194
LENGTH: 320
TYPE: DNA
ORGANISM: Homo sapiens
US-09-606-421B-194

Query Match 18.0%; Score 320; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 3.9e-90;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1399 CCCTTCCCAATCCATCAGTAAGACCCCATCTGCCCTTGTCCATGCCGTTTCCCAACAGGG 1458
DB 1 CCCTTCCCAATCCATCAGTAAGACCCCATCTGCCCTTGTCCATGCCGTTTCCCAACAGGG 60

QY 1459 ATGTCACCTTGATGAGAAATCTCAAAATCTCAATGCTTTATAGCAATTCCTCTGTGTC 1518
DB 61 ATGTCACCTTGATGAGAAATCTCAAAATCTCAATGCTTTATAGCAATTCCTCTGTGTC 120

QY 1519 ATTAAGACTCTGATAATTTGTCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATC 1578
DB 121 ATTAAGACTCTGATAATTTGTCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATC 180

QY 1579 CCCATCTCGGTTTCATATCAGAACTACCGTCCCGATATTCCTTCAGAGATTAAGA 1638
DB 181 CCCATCTCGGTTTCATATCAGAACTACCGTCCCGATATTCCTTCAGAGATTAAGA 240

QY 1639 CCAGAAAAAGTGAGCCCTTTCATCTGCACCTGTAAATAGTTTCAGTTCTTATTTCTTCC 1698
DB 241 CCAGAAAAAGTGAGCCCTTTCATCTGCACCTGTAAATAGTTTCAGTTCTTATTTCTTCC 300

QY 1699 ATTGACCCATATTTATACCT 1718
DB 301 ATTGACCCATATTTATACCT 320

RESULT 6
US-09-466-396A-194
Sequence 194, Application US/09466396A
Patent No. 6696247
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C4
CURRENT APPLICATION NUMBER: US/09/466,396A
CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 194
LENGTH: 320
TYPE: DNA
ORGANISM: Homo sapiens
US-09-466-396A-194

Query Match 18.0%; Score 320; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 3.9e-90;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1399 CCCTTCCCAATCCATCAGTAAGACCCCATCTGCCCTTGTCCATGCCGTTTCCCAACAGGG 1458
DB 1 CCCTTCCCAATCCATCAGTAAGACCCCATCTGCCCTTGTCCATGCCGTTTCCCAACAGGG 60

QY 1459 ATGTCACCTTGATGAGAAATCTCAAAATCTCAATGCTTTATAGCAATTCCTCTGTGTC 1518
DB 61 ATGTCACCTTGATGAGAAATCTCAAAATCTCAATGCTTTATAGCAATTCCTCTGTGTC 120

QY 1519 ATTAAGACTCTGATAATTTGTCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATC 1578
DB 121 ATTAAGACTCTGATAATTTGTCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATC 180

QY 1579 CCCATCTCGGTTTCATATCAGAACTACCGTCCCGATATTCCTTCAGAGATTAAGA 1638
DB 181 CCCATCTCGGTTTCATATCAGAACTACCGTCCCGATATTCCTTCAGAGATTAAGA 240

QY 1639 CCAGAAAAAGTGAGCCCTTTCATCTGCACCTGTAAATAGTTTCAGTTCTTATTTCTTCC 1698
DB 241 CCAGAAAAAGTGAGCCCTTTCATCTGCACCTGTAAATAGTTTCAGTTCTTATTTCTTCC 300

QY 1699 ATTGACCCATATTTATACCT 1718
DB 301 ATTGACCCATATTTATACCT 320

RESULT 7
US-09-476-496A-194
Sequence 194, Application US/09476496A
Patent No. 6706262
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Hosken, Nancy A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: LUNG CANCER
FILE REFERENCE: 210121.455C5
CURRENT APPLICATION NUMBER: US/09/476,496A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 254
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 194
LENGTH: 320
TYPE: DNA
ORGANISM: Homo sapiens
US-09-476-496A-194

Query Match 18.0%; Score 320; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 3.9e-90;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1399 CCCTTCCCAATCCATCAGTAAGACCCCATCTGCCCTTGTCCATGCCGTTTCCCAACAGGG 1458
DB 1 CCCTTCCCAATCCATCAGTAAGACCCCATCTGCCCTTGTCCATGCCGTTTCCCAACAGGG 60

QY 1459 ATGTCACCTTGATGAGAAATCTCAAAATCTCAATGCTTTATAGCAATTCCTCTGTGTC 1518
DB 61 ATGTCACCTTGATGAGAAATCTCAAAATCTCAATGCTTTATAGCAATTCCTCTGTGTC 120

QY 1519 ATTAAGACTCTGATAATTTGTCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATC 1578
DB 121 ATTAAGACTCTGATAATTTGTCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATC 180

QY 1579 CCCATCTCGGTTTCATATCAGAACTACCGTCCCGATATTCCTTCAGAGATTAAGA 1638
DB 181 CCCATCTCGGTTTCATATCAGAACTACCGTCCCGATATTCCTTCAGAGATTAAGA 240

QY 1639 CCAGAAAAAGTGAGCCCTTTCATCTGCACCTGTAAATAGTTTCAGTTCTTATTTCTTCC 1698
DB 241 CCAGAAAAAGTGAGCCCTTTCATCTGCACCTGTAAATAGTTTCAGTTCTTATTTCTTCC 300

QY 1699 ATTGACCCATATTTATACCT 1718
DB 301 ATTGACCCATATTTATACCT 320

RESULT 8

```
US-09-630-940B-194
; Sequence 194, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Ligu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 194
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-630-940B-194

Query Match
Best Local Similarity 18.0%; Score 320; DB 4; Length 320;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1399 CCCTTCCCAATCATCAGTAAGACCCCATCTGCTTGTCCATGCGTTTCCCAACAGGG 1458
Db 1 CCCTTCCCAATCATCAGTAAGACCCCATCTGCTTGTCCATGCGTTTCCCAACAGGG 60

QY 1459 ATGTCACTTGATGAGATCTCAATCTCAATGCTTATAGCATTCCTTCTCTGTCC 1518
Db 61 ATGTCACTTGATGAGATCTCAATCTCAATGCTTATAGCATTCCTTCTCTGTCC 120

QY 1519 ATTAAGACTCTGATATTTCTCTCCCTCCATAGGAATTTCTCCAGGAAGAAATATATC 1578
Db 121 ATTAAGACTCTGATATTTCTCTCCCTCCATAGGAATTTCTCCAGGAAGAAATATATC 180

QY 1579 CCCATCTCGTTTCATATCAGAACTACCTCCCGATATTCCTTCAGAGATTAAGA 1638
Db 181 CCCATCTCGTTTCATATCAGAACTACCTCCCGATATTCCTTCAGAGATTAAGA 240

QY 1639 CCAGAAAAGTGAGCTCTTCTATCTGCACCTGTAATAGTTTCAGTTCTTATTTCTTCC 1698
Db 241 CCAGAAAAGTGAGCTCTTCTATCTGCACCTGTAATAGTTTCAGTTCTTATTTCTTCC 300

QY 1699 ATTGACCCATATTTATACCT 1718
Db 301 ATTGACCCATATTTATACCT 320

RESULT 9
US-09-513-999C-8301
; Sequence 8301, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681

US-09-630-940B-194
; Sequence 194, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Ligu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 194
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-630-940B-194

Query Match
Best Local Similarity 18.0%; Score 320; DB 4; Length 320;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1399 CCCTTCCCAATCATCAGTAAGACCCCATCTGCTTGTCCATGCGTTTCCCAACAGGG 1458
Db 1 CCCTTCCCAATCATCAGTAAGACCCCATCTGCTTGTCCATGCGTTTCCCAACAGGG 60

QY 1459 ATGTCACTTGATGAGATCTCAATCTCAATGCTTATAGCATTCCTTCTCTGTCC 1518
Db 61 ATGTCACTTGATGAGATCTCAATCTCAATGCTTATAGCATTCCTTCTCTGTCC 120

QY 1519 ATTAAGACTCTGATATTTCTCTCCCTCCATAGGAATTTCTCCAGGAAGAAATATATC 1578
Db 121 ATTAAGACTCTGATATTTCTCTCCCTCCATAGGAATTTCTCCAGGAAGAAATATATC 180

QY 1579 CCCATCTCGTTTCATATCAGAACTACCTCCCGATATTCCTTCAGAGATTAAGA 1638
Db 181 CCCATCTCGTTTCATATCAGAACTACCTCCCGATATTCCTTCAGAGATTAAGA 240

QY 1639 CCAGAAAAGTGAGCTCTTCTATCTGCACCTGTAATAGTTTCAGTTCTTATTTCTTCC 1698
Db 241 CCAGAAAAGTGAGCTCTTCTATCTGCACCTGTAATAGTTTCAGTTCTTATTTCTTCC 300

QY 1699 ATTGACCCATATTTATACCT 1718
Db 301 ATTGACCCATATTTATACCT 320

RESULT 9
US-09-513-999C-8301
; Sequence 8301, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
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; SOFTWARE: Patent.pm
; SEQ ID NO 8301
; LENGTH: 162
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-8301

Query Match
Best Local Similarity 100.0%; Score 117; DB 4; Length 162;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCACAGTACCGCGCGGCCAGGCAATCCGACCAATTTCACTCTCACCCTGTAG 60
Db 46 AGCTCACAGTACCGCGCGGCCAGGCAATCCGACCAATTTCACTCTCACCCTGTAG 105

QY 61 GAATCCAGATGAGCCCAAGTATACAGCAGCAGGAGCATGCTGATGATGATGGG 117
Db 106 GAATCCAGATGAGCCCAAGTATACAGCAGCAGGAGCATGCTGATGATGATGGG 162

RESULT 10
US-08-690-095-2
; Sequence 2, Application US/08690095
; Patent No. 5792648
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,095
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: MPHNOT03
; CLONE: 513418
US-08-690-095-2

Query Match
Best Local Similarity 4.7%; Score 82.6; DB 1; Length 970;
Matches 145; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 383 CCAGATAATAAGCTTGCAGGAAGTTGCAGCATGTGGCTGAAAAAATCTTGTCTGAGCT 442
Db 443 CAAGATCAGGAACCTCTCCACCACACTGCAAAACATAGCCACCAATATTGTCTGAGCT 502

QY 443 GTATAAACAAGCTGGAGGACACAGCTGAGCCCTTGTACAGAACATGGAATGCGATG 502
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Db 503 ATATAGCAAGAACAGAGCAAAATGTAAGCCTTTGTCCAAGGAGATGGATTTGGCATAA 562
QY 503 AGACAATTGCTACCAAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAATATTCTG 562
Db 563 GGACAGCTGTTATTTCCCTAAGTGATGTCCAAACATGGCAGGAGAGTAATAATGCGCTG 622
QY 563 CTTAGTGAATACTTACCATCTGAAGATAAACAACAAGAACCTGGAAATTTGCGCGC 622
Db 623 TGCTGCTCAGATGCCAGCCTGTTGAAGATAAACAACAATAATGATTGGAATTTATAAA 682
QY 623 GTCTCAGAG 631
Db 683 ATCCAGAG 691

RESULT 11
US-09-113-789-2
; Sequence 2, Application US/09113789
; Patent No. 6034219
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,789
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/690,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: MPHGNOT03
; CLONE: 513418
US-09-113-789-2

Query Match 4.7%; Score 82.6; DB 3; Length 970;
Best Local Similarity 58.2%; Pred. No. 5.3e-15;
Matches 145; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY 383 CCAGAAATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAAATCTCTGTGCTGAGCT 442
Db 443 CAAGATCAGGAACCTCTCCACCACACTGCAACAATAGCCACCAATATATGTGCTGAGCT 502
QY 443 GTATAACAAAGCTGGAGCACAGCTGAGCCCTTGTACAGAACATGGAATGGCATGG 502

Db 503 ATATAGCAAGAACAGAGCAAAATGTAAGCCTTTGTCCAAGGAGATGGATTTGGCATAA 562
QY 503 AGACAATTGCTACCAAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAATATTCTG 562
Db 563 GGACAGCTGTTATTTCCCTAAGTGATGTCCAAACATGGCAGGAGAGTAATAATGCGCTG 622
QY 563 CTTAGTGAATACTTACCATCTGAAGATAAACAACAAGAACCTGGAAATTTGCGCGC 622
Db 623 TGCTGCTCAGATGCCAGCCTGTTGAAGATAAACAACAATAATGATTGGAATTTATAAA 682
QY 623 GTCTCAGAG 631
Db 683 ATCCAGAG 691

RESULT 12
US-09-016-434-800
; Sequence 800, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 800:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: MPHGNOT03
; CLONE: 513418
US-09-016-434-800

Query Match 4.7%; Score 82.6; DB 4; Length 970;
Best Local Similarity 58.2%; Pred. No. 5.3e-15;
Matches 145; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY 383 CCAGAAATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAAATCTCTGTGCTGAGCT 442
Db 443 CAAGATCAGGAACCTCTCCACCACACTGCAACAATAGCCACCAATATATGTGCTGAGCT 502
QY 443 GTATAACAAAGCTGGAGCACAGCTGAGCCCTTGTACAGAACATGGAATGGCATGG 502

Db 503 ATATAGCAAGAACAAGACCAAAATGTAAGCTTTGTCCCAAGGAGATGGATTTGGCATAA 562
QY 503 AGACAAATTCCTACCGATTTCTATAAGACAGACAAAAGTTGGGAGGACTGTAAATATTTCTG 562
Db 563 GGACAGCTGTTATTTCTTAAGTGATGTGTCCAAACATGGCAGGAGGTAAAATGGCCTG 622
QY 563 CCTAGTGAAGAACTCTACCATCTGAAGATAAACAACAAGACCTGGAATTTGGCCG 622
Db 623 TGCTGCTCAGATGCCAGCTGTTGAAGATAAACAACAATAATGCATTGGAATTTATAAA 682
QY 623 GTCTCAGAG 631
Db 683 ATCCCAGAG 691

RESULT 13
US-09-482-273-34
; Sequence 34, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; CURRENT FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 1737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1674)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1731)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-482-273-34

Query Match 4.7%; Score 82.6; DB 4; Length 1737;
Best Local Similarity 58.2%; Pred. No. 8e-15;
Matches 145; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY 383 CCAGAAATATAAGCTTGCAGGAAGTCTGCAGCATGGCTGAAACAACTCTGTCGTGAGCT 442
Db 495 CAAGATCAGGAACCTCTCCACACACTGCAAAATAGCACCAAAATATATGTCGTGAGCT 554
QY 443 GTATAACAAGCTGGAGACACAGGTGCGCCCTTTGTACAGAACAAATGGAATGGCATGG 502
Db 555 ATATAGCAAGAACAAGACCAAAATGTAAGCTTTGTCCCAAGGAGATGGATTTGGCATAA 614
QY 503 AGACAAATTCCTACCGATTTCTATAAGACAGACAAAAGTTGGGAGGACTGTAAATATTTCTG 562
Db 615 GGACAGCTGTTATTTCTTAAGTGATGTGTCCAAACATGGCAGGAGGTAAAATGGCCTG 674
QY 563 CCTAGTGAAGAACTCTACCATCTGAAGATAAACAACAAGACCTGGAATTTGGCCG 622
Db 675 TGCTGCTCAGATGCCAGCTGTTGAAGATAAACAACAATAATGCATTGGAATTTATAAA 734
QY 623 GTCTCAGAG 631
Db 735 ATCCCAGAG 743

RESULT 14
US-09-976-594-1045
; Sequence 1045, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 1045
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 406707.2
; NAME/KEY: unsure
; LOCATION: 459, 463
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-1045

Query Match 3.8%; Score 67.8; DB 4; Length 505;
Best Local Similarity 50.3%; Pred. No. 1.5e-10;
Matches 218; Conservative 0; Mismatches 209; Indels 6; Gaps 2;
QY 315 CAAGACACCATTTCTCAAAATGGAAGAAAGATTAGGAATACGTCCCAAGAGTTGCATCT 374
Db 67 CAGGATAAATCTATCCAGCAACTGGGCAACTCCAACTTGTCTCATGGAGGAGGAATTT 126
QY 375 CTTCAAGTCCAGATATAAAGCTTGCAGGAAGTGTGCAGCATGTGGCTGAAAACTCTCT 434
Db 127 CTTCAAGTCCAGATCTCCAGTCTACTGAAGAGGAGGAACAATGGCCATCAACTGTGC 186
QY 435 COTGAGCTGTATAACAAGCTGGAGCACACAGGTGAGCCCTTGTACAGAACAAATGGAAA 494
Db 187 CAAGAGCTAATCATTCATACCTTCAGACACAGATGTAATCCATGCTTAAGATGTGCAA 246
QY 495 TGGCATGGAGACAATGTCTACAGTTCTATAAA---GACAGCAAAAGTTGGGAGGACTGT 551
Db 247 TGGTACCAAAATAGTTGCTACTATTTTACAACAAAATGAGGAGAAAACCTGGGCTAAC 306
QY 552 AAATATTTCTGCTTAGTGAAACCTCTACCATGCTGAAGATAAACAACAAGACCTG 611
Db 307 AGAAAGGACTGCATAGACAAGAACTCCACCTTAGTGAAGATAGACAGTTTGGAAAGAAAG 366
QY 612 GAATTTGGCGGCTCTCAGAGCTACTCTGAGTTTTTTCTACTTTTATTTGGACAGGCTTTTG 671
Db 367 GATTTTCTTATGTACAGCCATTAATCTATGTTTTCGTTTCTTTCGTTTCTTTCGTTTCT 423
QY 672 CGCCCTGACAGTGGCAAGCCCTGGCTGTGGATGGATGGAAACCCCTTTTCACTTCTGAACTG 731
Db 424 TGGGACTCTCTGGCAGAAAGTTGGTTCTGGGAAGANGCNCCTGTTCCCTCTCCACTCTG 483
QY 732 TTCCATATTATAA 744
Db 484 TACGCTCTCCTAA 496

RESULT 15
US-08-688-342-2
; Sequence 2, Application US/08688342
; Patent No. 5871964
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goli, Surya K.

Search completed: October 8, 2005, 00:39:11
Job time : 332 secs


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; APPLICATION NUMBER: US/09/746,783
; FILING DATE: 21-Dec-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Milasincic, Debra J.
; REGISTRATION NUMBER: 46,931
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1776 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; SEQUENCE DESCRIPTION: SEQ ID NO: 159:
US-09-746-783-159

Query Match          100.0%; Score 1776; DB 10; Length 1776;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCACAGTAGCCCGGGGCCAGGCAATCCGACCAATTTCACTCTCACCGCTGTAG 60
DB 1 AGCTCACAGTAGCCCGGGGCCAGGCAATCCGACCAATTTCACTCTCACCGCTGTAG 60

QY 61 GAATCCAGATGAGCCCAAGTACAGCAGCAGAGGGAATGCTGGATGATGATGGGACA 120
DB 61 GAATCCAGATGAGCCCAAGTACAGCAGCAGAGGGAATGCTGGATGATGATGGGACA 120

QY 121 CCACCATGAGCTGCAATCTCAAGCTCTGCCAATCTCGGCATCCGAGCCCGGGCCA 180
DB 121 CCACCATGAGCTGCAATCTCAAGCTCTGCCAATCTCGGCATCCGAGCCCGGGCCA 180

QY 181 CAGAGCACAGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCTGCTGACTTTGT 240
DB 181 CAGAGCACAGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCTGCTGACTTTGT 240

QY 241 GCTTGGTCTGTATAGGGCTGGCAGCCCTGGGGCTTTTGTCTTTCAGTACTACGAGC 300
DB 241 GCTTGGTCTGTATAGGGCTGGCAGCCCTGGGGCTTTTGTCTTTCAGTACTACGAGC 300

QY 301 TCTCCAACTACTGGTCAAGACACATTTCTCAAATGGAAGAAAGATTAGAAATAGCTCCC 360
DB 301 TCTCCAACTACTGGTCAAGACACATTTCTCAAATGGAAGAAAGATTAGAAATAGCTCCC 360

QY 361 AAGAGTTGCAATCTCTTCAAGTCCAGAAATATAAAGCTTGCAGGAAAGTCTGCAGCATGTGG 420
DB 361 AAGAGTTGCAATCTCTTCAAGTCCAGAAATATAAAGCTTGCAGGAAAGTCTGCAGCATGTGG 420

QY 421 CTGAAAAACTCTGCTGAGCTGTATACAAAGCTGGAGGACACAGGTGCGAGCCCTTGTGTA 480
DB 421 CTGAAAAACTCTGCTGAGCTGTATACAAAGCTGGAGGACACAGGTGCGAGCCCTTGTGTA 480

QY 481 CAGAAATGAAATGGCATGGAGCAATTTGCTACAGTTCTATAAAGACAGCAAAAGTT 540
DB 481 CAGAAATGAAATGGCATGGAGCAATTTGCTACAGTTCTATAAAGACAGCAAAAGTT 540

QY 541 GGGAGGACTGAAATATTTCTGCTTGTAGTAAACTCTACCATGCTGAAGATAAACAAC 600
DB 541 GGGAGGACTGAAATATTTCTGCTTGTAGTAAACTCTACCATGCTGAAGATAAACAAC 600

QY 601 AAGAGACCTGGAATTTGCGCGCTCAGAGCTACTCTGAGTTTTCCTTCTTATTTGGA 660
DB 601 AAGAGACCTGGAATTTGCGCGCTCAGAGCTACTCTGAGTTTTCCTTCTTATTTGGA 660

QY 661 CAGGCTTTTGGCCCTGACAGTGCAGAGGCTGCTGGATGATGATGAAACCCCTTTCA 720
DB 661 CAGGCTTTTGGCCCTGACAGTGCAGAGGCTGCTGGATGATGATGAAACCCCTTTCA 720

QY 721 CTTCTGAACTGTTCATATTAATAGATGTCCAGGCCCAAGAGCAGAGACTGTGTGG 780
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RESULT 2

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DB 721 CTTCTGAACTGTTCATATTAATAGATGTCCAGGCCCAAGAGCAGAGACTGTGTGG 780
QY 781 CCATCCTTAATGGGATGATCTTCTCAAGGAGCTGCAAGAAATTTGAAGGCTGTGTCTGTG 840
DB 781 CCATCCTTAATGGGATGATCTTCTCAAGGAGCTGCAAGAAATTTGAAGGCTGTGTCTGTG 840
QY 841 AGAGAAGGGCAGGAATGGTGAAGCAGAGAGCGCTCCATGTCCCCCTCAAAACATTAGGCG 900
DB 841 AGAGAAGGGCAGGAATGGTGAAGCAGAGAGCGCTCCATGTCCCCCTCAAAACATTAGGCG 900
QY 901 AAGGTGACTGATCGCCCTCTGCAACTCAAAATAGCAGAGTGAGCCGGTGCCAAAG 960
DB 901 AAGGTGACTGATCGCCCTCTGCAACTCAAAATAGCAGAGTGAGCCGGTGCCAAAG 960
QY 961 CAAGGGCTAGTTGAGACATTTGGGAAATGGAACATAATCAGGAAAGACTATCTCTGTACT 1020
DB 961 CAAGGGCTAGTTGAGACATTTGGGAAATGGAACATAATCAGGAAAGACTATCTCTGTACT 1020
QY 1021 AGTACAAAATGGGTTCTCGTGTTCCTGTTTCAGGATCACAGCATTTCTGAGCTTGGGTT 1080
DB 1021 AGTACAAAATGGGTTCTCGTGTTCCTGTTTCAGGATCACAGCATTTCTGAGCTTGGGTT 1080
QY 1081 TATGCACTATTTTAAACAGTCAAGAAGTCTTATTTACATGCCCAACCAACCTCAGAA 1140
DB 1081 TATGCACTATTTTAAACAGTCAAGAAGTCTTATTTACATGCCCAACCAACCTCAGAA 1140
QY 1141 ACCCATATGTCATCTGCTTCTTGGCTTAGAGATACTTTTAGCTCTCTTCTCTCAA 1200
DB 1141 ACCCATATGTCATCTGCTTCTTGGCTTAGAGATACTTTTAGCTCTCTTCTCTCAA 1200
QY 1201 TGTCTAATATCACCTCCCTGTTTTTCATGTCCTTCTTACATTTGGTGAATTAAGAACTTT 1260
DB 1201 TGTCTAATATCACCTCCCTGTTTTTCATGTCCTTCTTACATTTGGTGAATTAAGAACTTT 1260
QY 1261 TTGAAGTAGAGGAAATACATTTGAGGTAACTCTTCTCTGACAGTCAAGTAGTCCATC 1320
DB 1261 TTGAAGTAGAGGAAATACATTTGAGGTAACTCTTCTCTGACAGTCAAGTAGTCCATC 1320
QY 1321 AGAAATTTGGCAGTCACTTCCAGATTTGACAGCAAAATACACAGGAAATCTTTTTGTTT 1380
DB 1321 AGAAATTTGGCAGTCACTTCCAGATTTGACAGCAAAATACACAGGAAATCTTTTTGTTT 1380
QY 1381 GTTTTCAGTTTCATCTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTTGTCCA 1440
DB 1381 GTTTTCAGTTTCATCTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTTGTCCA 1440
QY 1441 TGCGGTTTCCCAACAGGGATGTCACTTGGATATGAGAATCTCAATCTCAATGCTTTATAA 1500
DB 1441 TGCGGTTTCCCAACAGGGATGTCACTTGGATATGAGAATCTCAATCTCAATGCTTTATAA 1500
QY 1501 GCATTTCTCTGTCCTCAATTAAGACTCTGATAATTTGTCCTCCCTCCATAGGAATTTCTC 1560
DB 1501 GCATTTCTCTGTCCTCAATTAAGACTCTGATAATTTGTCCTCCCTCCATAGGAATTTCTC 1560
QY 1561 CCAGGAAAGAAATATATCCCATCTCCGTTTTCATATCAGAACTACCGTCCCGGATATTCC 1620
DB 1561 CCAGGAAAGAAATATATCCCATCTCCGTTTTCATATCAGAACTACCGTCCCGGATATTCC 1620
QY 1621 CTTCAGAGAGATTAAGACCAAGAAAAGTGAAGCTCTTCAATCTGCACTGTATAAGTTT 1680
DB 1621 CTTCAGAGAGATTAAGACCAAGAAAAGTGAAGCTCTTCAATCTGCACTGTATAAGTTT 1680
QY 1681 CAGTTCTCTATTTTCTTCCATTTGACCCATTTATATACCTTTTTCAGGTACTGAAATTAATA 1740
DB 1681 CAGTTCTCTATTTTCTTCCATTTGACCCATTTATATACCTTTTTCAGGTACTGAAATTAATA 1740
QY 1741 ATAATAAATGTAAATACTGTGCAAAAAAATAAAAAA 1776
DB 1741 ATAATAAATGTAAATACTGTGCAAAAAAATAAAAAA 1776
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US-09-989-722-318
; Sequence 318, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
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; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
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; PRIOR FILING DATE: 1998-06-09
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
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; PRIOR FILING DATE: 1998-06-16
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; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355

[illegible]

Db 1336 TTGAGTAGAGGAATACATTGAGGTAAACATCCTTTTCTGACAGTCAAGTAGTCCATC 1395
QY 1321 AGAATTTGGCAGTCACTTCCGAGATTGTACCGAAATACACAAGGAATCTTTTGTGTT 1380
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QY 1381 GTTTCAGTTTCATCTAGTCCCTTCCCAATCCATCAGTAAGACCCCATCTGCTTTGTCCA 1440
Db 1456 GTTTCAGTTTCATCTAGTCCCTTCCCAATCCATCAGTAAGACCCCATCTGCTTTGTCCA 1515
QY 1441 TGCCGTTTCCCAACAGGAGTGTCACTTGATATGAGAAATCTCAATCTCAATGCTTATAA 1500
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Db 1576 GAATTCCTTCTGTGTCATTAAGACTCTGATAATTTGTCTCCCTCCCATAGGAATTTCTC 1635
QY 1561 CCAGGAAGAATATATATCCCATCTCCGTTTCATATCAGAACTACCGTCCCGATATTC 1620
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QY 1681 CAGTTCCTATTTTCTTCCATGACCCATATTTATACCTTTCAGGTACTGAAGATTAAATA 1740
Db 1756 CAGTTCCTATTTTCTTCCATGACCCATATTTATACCTTTCAGGTACTGAAGATTAAATA 1815
QY 1741 ATAATAAATGTAATCTGTGAAAAA 1766
Db 1816 ATAATAAATGTAATCTGTGAAAAA 1841

RESULT 3

US-09-989-723-318

; Sequence 318, Application US/09989723

; Patent No. US20020072092A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730PIC62

; CURRENT APPLICATION NUMBER: US/09/989,723

; CURRENT FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
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; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
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; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512

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	; PRIOR FILING DATE: 1998-07-01	
	; PRIOR APPLICATION NUMBER: 60/091478	
	; PRIOR FILING DATE: 1998-07-02	
	; PRIOR APPLICATION NUMBER: 60/091544	
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	; PRIOR APPLICATION NUMBER: 60/091633	
	; PRIOR FILING DATE: 1998-07-02	
	; PRIOR APPLICATION NUMBER: 60/091978	
	; PRIOR FILING DATE: 1998-07-07	
	; PRIOR APPLICATION NUMBER: 60/091982	
	; PRIOR FILING DATE: 1998-07-07	
	; PRIOR APPLICATION NUMBER: 60/092182	
	; PRIOR FILING DATE: 1998-07-09	
	Query Match 99.3%; Score 1764.4; DB 9; Length 1841;	
	Best Local Similarity 99.9%; Pred. No. 0;	
	Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 AGCTCAGTAGCCCGCGGCCACGAGGCATTCGACCACATTTCCACTCTCACCGCTGTAG 60	
Dd	76 AGCTCAGTAGCCCGCGGCCACGAGGCATTCGACCACATTTCCACTCTCACCGCTGTAG 135	
Qy	61 GAATCCAGATGCAGGCCCAAGTACAGCAGCAGAGGGACATGCTGGATGATGATGGGACA 120	
Dd	136 GAATCCAGATGCAGGCCCAAGTACAGCAGCAGAGGGACATGCTGGATGATGATGGGACA 195	
Qy	121 CCACCATGAGCCCTGCATTCTCAAGCCTCTGCCAACTCGGCATCCAGAGCCCCGGCGCA 180	
Dd	196 CCACCATGAGCCCTGCATTCTCAAGCCTCTGCCAACTCGGCATCCAGAGCCCCGGCGCA 255	
Qy	181 CAGAGCACAGGGCTCCCTCTTCAAAGCTGGCGGACAGAGTGCCCTGACCCCTGCTGACTTTGT 240	
Dd	256 CAGAGCACAGGGCTCCCTCTTCAAAGCTGGCGGACAGAGTGCCCTGCTGACTTTGT 315	
Qy	241 GCCTTGGTGCCTGTGATAGGGCTGCGAGCCCTGGSGCTTTTGTTTTTTTCAGTACTACCAAGC 300	
Dd	316 GCCTTGGTGCCTGTGATAGGGCTGCGAGCCCTGGSGCTTTTGTTTTTTTCAGTACTACCAAGC 375	
Qy	301 TCTCCAATACTGGTCAAGACACCATTTCTCAAATGGGAAGAAGATTAGGAATAACGTCCC 360	
Dd	376 TCTCCAATACTGGTCAAGACACCATTTCTCAAATGGGAAGAAGATTAGGAATAACGTCCC 435	
Qy	361 AAGAGTTGCAATCTCTTCAAAGTCCAGAAATATAAAGCTTGCAGGAAGCTCTGCAGCATGTGG 420	
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Qy	541 GGGAGGACTGTAAATATTTCTGCCCTTAGTGAAAACTCTTACCATGCTGAAGATAAACAAC 600	
Dd	616 GGGAGGACTGTAAATATTTCTGCCCTTAGTGAAAACTCTTACCATGCTGAAGATAAACAAC 675	
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Dd	676 AAGNAGACCTGGAAATTTGCCGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGA 735	
Qy	661 CAGGGCTTTTGGCCCTTGACAGTGGCAAGGCCTGGCTGTGATGGATGGAACCCCTTTCA 720	
Dd	736 CAGGGCTTTTGGCCCTTGACAGTGGCAAGGCCTGGCTGTGATGGATGGAACCCCTTTCA 795	
Qy	721 CTTCTGAACCTGTTCCATATTATTAATAGATGTACCAAGCCCAAGACGAGACTGTGTGG 780	

Db 796 CTTCTCAACTGTTCCATATTATTAATAGATGTACACAGCCCAAGAACGACGAGCTGTGGT 855
Qy 781 CCATCTTAAATGGGATGATCTTCTCAAGAGATGCGAAAGAAATGGAAGCGTTGTCTGTG 840
Db 856 CCATCTTCAATGGGATGATCTTCTCAAGAGACTGCAAGAAATGGAAGCGTTGTCTGTG 915
Qy 841 AGAAGAGGGCAGGAATGGTGAAGCCAGAGAGCTCCATGTGCCCTCGAAACATTAGGCG 900
Db 916 AGAAGAGGGCAGGAATGGTGAAGCCAGAGAGCTCCATGTGCCCTCGAAACATTAGGCG 975
Qy 901 AAGGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGCGGTGCGCAAG 960
Db 976 AAGGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGCGGTGCGCAAG 1035
Qy 961 CAAGGCTAGTTAGACATTTGGGAATGGAACATAATCAGGAAGACTATCTCTGTGACT 1020
Db 1036 CAAGGCTAGTTAGACATTTGGGAATGGAACATAATCAGGAAGACTATCTCTGTGACT 1095
Qy 1021 AGTACAAAATGGGTTCTCGTGTCTCTGTTTCCAGGATCACAGCATTTCTGAGCTTGGGTT 1080
Db 1096 AGTACAAAATGGGTTCTCGTGTCTCTGTTTCCAGGATCACAGCATTTCTGAGCTTGGGTT 1155
Qy 1081 TATGCAAGTATTAAACAGTCACAAGAGTCTTATTTACATGCCCAACCAACCTCAGAA 1140
Db 1156 TATGCAAGTATTAAACAGTCACAAGAGTCTTATTTACATGCCCAACCAACCTCAGAA 1215
Qy 1141 ACCATAATGTGATCTGCTCTCTTGGCTTAGAGATAAATCTTTAGCTCTCTTCTCTCAA 1200
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Qy 1201 TGTCTAATATCACTCCCTGTTTTCATGCTCTTCTTACACTTGGTGAATAGAACTTT 1260
Db 1276 TGTCTAATATCACTCCCTGTTTTCATGCTCTTCTTACACTTGGTGAATAGAACTTT 1335
Qy 1261 TTGAAGTAGAGGAATATACATTTAGGTAAATCTTTCTCTGACAGTCAAGTAGTCCATC 1320
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Db 1396 AGAAATGGCAGTCACTTCCAGATTTGTAACGAAATACAAAGAAATCTTTTGTGTT 1455
Qy 1381 GTTTCAGTTTCATAGTCCCTTCCCAATCCATCAGTAAGACCCCATCTGCTTGTCCA 1440
Db 1456 GTTTCAGTTTCATAGTCCCTTCCCAATCCATCAGTAAGACCCCATCTGCTTGTCCA 1515
Qy 1441 TGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAAATCTCAAAATCTCAATGCCATTAA 1500
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Qy 1561 CCAGGAAGAAATATATATCCCATCTCCGTTTCTATATCAGAACTACCGTCCCGATATCC 1620
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Db 1816 ATAATAAATGTAATACTGTGAAAA 1841

RESULT 4

US-09-989-279-318

; Sequence 318, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 1764.4; DB 9; Length 1841;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 136 GAATCCAGATGCGAGCCCAAGTACAGCAGCAGGGACATGCTGGATGATGATGGGACA 195

Qy 121 CCACATGAGCTGCATTCTCAAGCCTCTGCAACAATCCGATCCAGAGCCCGCGCGCA 180

Db 196 CCACATGAGCTGCATTCTCAAGCCTCTGCAACAATCCGATCCAGAGCCCGCGCGCA 255

Qy 181 CAGAGCACAGGGCTCCCTCTTTCAAACGTGGGCGACAGGTGGCCCTGACCTCTGTACTTTGT 240

Db 256 CAGAGCACAGGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCCCTGCTGACTTGT 315
Qy 241 GCTTGGTGTCTGTATAGGGCTGGCAGCCCTGGGGCTTTTGTGTTTTCAGTACTACAGC 300
Db 316 GCTTGGTGTCTGTATAGGGCTGGCAGCCCTGGGGCTTTTGTGTTTTCAGTACTACAGC 375
Qy 301 TCTCCAAATCTGCTCAAGACACCATTTCTCAATATGGAAGAAAGATTAGGAATACGTCC 360
Db 376 TCTCCAAATCTGCTCAAGACACCATTTCTCAATATGGAAGAAAGATTAGGAATACGTCC 435
Qy 361 AAGAGTTGCAATCTCTTCAAGTCCAGAATATAAGCTTGCAGGAAGTCTGCAGCATGTGG 420
Db 436 AAGAGTTGCAATCTCTTCAAGTCCAGAATATAAGCTTGCAGGAAGTCTGCAGCATGTGG 495
Qy 421 CTGAAAACTCTGCTGAGCTGTATATAAAGCTGTGAGCAACAGGTGCGAGCCCTTGTGA 480
Db 496 CTGAAAACTCTGCTGAGCTGTATATAAAGCTGTGAGCAACAGGTGCGAGCCCTTGTGA 555
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Db 556 CAGAACAATGGAAATGGCATGGAGCAATTTGCTACCAAGTCTTATAAGACAGCAAAAGTT 615
Qy 541 GGGAGGACTGTAAATATTTCTGCCCTTAGTGAATCTTACCATGCTGGAAGATAAACAAC 600
Db 616 GGGAGGACTGTAAATATTTCTGCCCTTAGTGAATCTTACCATGCTGGAAGATAAACAAC 675
Qy 601 AAGAGACCTGGAAATTTGCGCGTCTCAGAGCTACTCTGAGTTTTTCTTACTCTTATGGA 660
Db 676 AAGAGACCTGGAAATTTGCGCGTCTCAGAGCTACTCTGAGTTTTTCTTACTCTTATGGA 735
Qy 661 CAGGCTTTTGGCCCTGACAGTGGCAGAGCCCTGCTGGATGATGGAACCCCTTCA 720
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Db 796 CTCTGAACTGTTCATATTAATAGATGTCAACAGCCCAAGAGCAGAGACTGTGTGG 855
Qy 781 CCACTCTTAATGGAGTATCTTCTCAAGGACTGCAAGAAATGGAAGCTGTGTGTG 840
Db 856 CCACTCTTAATGGAGTATCTTCTCAAGGACTGCAAGAAATGGAAGCTGTGTGTG 915
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Qy 1141 ACCCAATATGCTATGCTCTTGGCTTATGAGTAACTTTTCTGCTCTTCTTCTCAA 1200
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Db 1456 GTTTCAGTTCATACTAGTCCCTTCCCAATCATCAGTAAAGACCCCATCTGCTTGTCCA 1515
Qy 1441 TGCGGTTTCCCAACAGGATGCTCTTCAATGAGAATCTCAATCTCAATGCTTATTA 1500
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Db 1756 CAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTGAGTACTGAAGATTTAATA 1815
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Db 1816 ATAAATAATGTAATACTGTGAAAA 1841

RESULT 5

US-09-989-727-318

; Sequence 318 Application US/09989727

; Patent No. US20020072497A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730PlC65

; CURRENT APPLICATION NUMBER: US/09/989,727

; PRIORITY FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

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;; PRIOR FILING DATE: 1998-07-01
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 1764.4; DB 9; Length 1841;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTCAGTAGCCCGCGGCCAGGGCAATCCGACCAATTTCACTCTCACCGCTGTAG 60
DB 76 AGCTCAGTAGCCCGCGGCCAGGGCAATCCGACCAATTTCACTCTCACCGCTGTAG 135

QY 61 GAATCCAGATGACGGCCAAAGTACAGACGACGAGGACATGCTGGATGATGAGGACA 120
DB 136 GAATCCAGATGACGGCCAAAGTACAGACGACGAGGACATGCTGGATGATGAGGACA 195

QY 121 CCACCATGAGCTGCATTTCTCAAGCTCTGCCCACTCGGCATCCAGAGCCCGCGCA 180
DB 196 CCACCATGAGCTGCATTTCTCAAGCTCTGCCCACTCGGCATCCAGAGCCCGCGCA 255

QY 181 CAGAGCACAGGGCTCCCTCTTCAAAGTGGCGACAGTGGCCCTGACCTGCTGACTTTGT 240
DB 256 CAGAGCACAGGGCTCCCTCTTCAAAGTGGCGACAGTGGCCCTGACCTGCTGACTTTGT 315

QY 241 GCTTGGTGTCTGTAGTGGCTGGAGCCCTGGGGCTTTTGTTCAGTACTACACAGC 300
DB 316 GCTTGGTGTCTGTAGTGGCTGGAGCCCTGGGGCTTTTGTTCAGTACTACACAGC 375

QY 301 TCTCCAAATCTGGTCAAGACACATTTCTCAATGGAAGAAAGATTAGGAATAGTCCC 360
DB 376 TCTCCAAATCTGGTCAAGACACATTTCTCAATGGAAGAAAGATTAGGAATAGTCCC 435

QY 361 AAGAGTTGCAATCTCTTCAAGTCCAGAAATATAAGCTTGCAGGAAGTCTGCAGCATGTGG 420
DB 436 AAGAGTTGCAATCTCTTCAAGTCCAGAAATATAAGCTTGCAGGAAGTCTGCAGCATGTGG 495

QY 421 CTGAAAAAATCTGTCTGTAGCTGTATAACAAAGCTGGAGACACAGGTGACGCCCTTGA 480
DB 496 CTGAAAAAATCTGTCTGTAGCTGTATAACAAAGCTGGAGACACAGGTGACGCCCTTGA 555

QY 481 CAGAACAAATGGAAATGGCATGGACAAATTTGTACAGTTCTATAAGACAGCAAAAGTT 540
DB 556 CAGAACAAATGGAAATGGCATGGACAAATTTGTACAGTTCTATAAGACAGCAAAAGTT 615

QY 541 GCGAGGACTGTAATATTTCTGCTTAGTGAATACTTACCATGCTGAAGATAAACAAC 600
DB 616 GCGAGGACTGTAATATTTCTGCTTAGTGAATACTTACCATGCTGAAGATAAACAAC 675

QY 601 AAGAGACCTGGAATTTGCCGCTCTCAGAGTACTCTGAGTTTTTCTACTTTATGGA 660
DB 676 AAGAGACCTGGAATTTGCCGCTCTCAGAGTACTCTGAGTTTTTCTACTTTATGGA 735

QY 661 CAGGGCTTTTGGCCCTGACAGTGGCAAGCCCTGGCTGGATGATGGAACCCCTTCA 720
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QY 721 CTTCTGAATCTGTTCCATATTTATAATAGATGTCAACAGCCCAAGAGACAGAGCTGTGG 780
DB 796 CTTCTGAATCTGTTCCATATTTATAATAGATGTCAACAGCCCAAGAGACAGAGCTGTGG 855

RESULT 6

US-09-989-731-318

; Sequence 318, Application US/09989731

Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P27301PC70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
PRIORITY APPLICATION NUMBER: 60/049787
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 1764.4; DB 9; Length 1841;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCTCACAGTACCGGGGGCCAGGGCAATCCGACCAATTTCACTCTCACCGCTGTAG 60
DB 76 ACCTCACAGTACCGGGGGCCAGGGCAATCCGACCAATTTCACTCTCACCGCTGTAG 135

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DB 256 CAGAGCACAGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCTGCTGACTTTGT 315

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DB 736 CAGGGCTTTTGGCCCTGACAGTGCAGAGGCTGTGGATGATGGAACCCCTTTTCA 795

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DB 796 CTTCTGAACCTGTTCATATTAATAGATGTCAACAGCCCAAGAGACAGAGACTGTGTGG 855

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Db 1816 ATAATAATGTAAATACGTGGAARA 1841

RESULT 7

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; Sequence 318, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLC57
; CURRENT APPLICATION NUMBER: US/09/989,732
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; Patent No. US20020132252A1
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PlC8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-07-07
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; Patent No. US20020132253A1
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC17
CURRENT APPLICATION NUMBER: US/09/991,163
CURRENT FILING DATE: 2001-11-14
PRIORITY APPLICATION NUMBER: 60/049787
PRIORITY FILING DATE: 1997-06-16
PRIORITY APPLICATION NUMBER: 60/062250
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PRIORITY FILING DATE: 1997-11-12
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PRIORITY FILING DATE: 1997-11-13
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PRIORITY FILING DATE: 1998-02-25
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PRIORITY FILING DATE: 1998-06-23
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PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: 60/090431

[illegible]

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Db 1516 TGCCGTTTCCCAACAGGATGTCACCTGTATGATGAGAACTCAATCTCAATGCTTATAA 1575
QY 1501 GCATTCCTTCTGTGTCATTAAGACTCTGATAATTTGTCTCCCTCCATAGGAATTTCTC 1560
Db 1576 GCATTCCTTCTGTGTCATTAAGACTCTGATAATTTGTCTCCCTCCATAGGAATTTCTC 1635
QY 1561 CAGGAAGAATATATATCCCATCTCCGTTTCATATCAGAACTACGTCCTCCGATATCC 1620
Db 1636 CAGGAAGAATATATATCCCATCTCCGTTTCATATCAGAACTACGTCCTCCGATATCC 1695
QY 1621 CTTTCAGAGATTTAAAGACCAGAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTT 1680
Db 1696 CTTTCAGAGATTTAAAGACCAGAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTT 1755
QY 1681 CAGTTCCTATTTTCTTCCATTTGACCCATATTTATATCTTTTCAGGTACTGAAGATTTATA 1740
Db 1756 CAGTTCCTATTTTCTTCCATTTGACCCATATTTATATCTTTTCAGGTACTGAAGATTTATA 1815
QY 1741 ATAATAATGTAATACTGTGAAAA 1766
Db 1816 ATAATAATGTAATACTGTGAAAA 1841

RESULT 11

US-09-993-604-318
; Sequence 318, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
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; PRIOR FILING DATE: 1998-06-16
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; PRIOR APPLICATION NUMBER: 60/089532

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Db 976 AAGGTGACTGATTCGCGCTCTGCAACTCAAAATAGCAGAGTGAAGCGGTGCAAG 1035
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Db 1276 TGCTTAATATCACTCCCTGTTTTCATGTCTTCTTCACTTGGTGGAAATAGAACTTTT 1335
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Db 1816 ATAATAAATGTAATCTGTGAAAA 1841

RESULT 12

US-09-990-456-318

; Sequence 318, Application US/09990456

; Patent No. US20020137890A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730F1C22
; CURRENT APPLICATION NUMBER: US/09/990,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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Db 976 AAGGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGATGAGCCGCGTGCAGAA 1035
Qy 961 CAAAGGCTAGTTGAGACATTTGGGAAATGGAACATAATCAGGAAGACTATCTCTGACT 1020
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Db 1276 TGCTTAATATACCTCCCTGTTTTTCATGTTCTTCTTACACTTTGGTGGAAATAGAAACTTT 1335
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Db 1336 TTGAAGTAGAGAAATACATTTGAGTAACTCTTTCTCTGACAGTCAAGTAGTCCATC 1395
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Db 1756 CAGTTCTTATTTTCTTCCATTCGACCATATTTATACCTTTTCAGGTACTGAAGATTTAATA 1815
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Db 1816 ATAATAATGTAATACTGTGAAAAA 1841

RESULT 13

US-09-989-721-318
; Sequence 318, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC55
; CURRENT APPLICATION NUMBER: US/09/989,721
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770

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;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 1764.4; DB 9; Length 1841;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	AGCTCAGTACGCGCGCGCCAGGCAATCCGACCAATTCACATTCCTCACCCTGTAG	60
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QY	61	GAATCCAGATGCGGCGCAAGTACAGCAGCAGGAGACATGCTGGATGATGAGGACA	120
DB	136	GAATCCAGATGCGGCGCAAGTACAGCAGCAGGAGACATGCTGGATGATGAGGACA	195
QY	121	CCACATGAGCCTGCAATTCCTAAGCCTCTGACCACTCGGATCCAGAGCCCGCGCA	180
DB	196	CCACATGAGCCTGCAATTCCTAAGCCTCTGACCACTCGGATCCAGAGCCCGCGCA	255
QY	181	CAGAGCAGGCGCTCCCTCTTCAAGTGGCGACAGTGGCCCTGACCTGCTGCTTGT	240
DB	256	CAGAGCAGGCGCTCCCTCTTCAAGTGGCGACAGTGGCCCTGACCTGCTGCTTGT	315
QY	241	GCTTGGTGTCTGATAGGCTGGCAGCCTCGGCGCTTTGTTTTTCACTACTACGAC	300
DB	316	GCTTGGTGTCTGATAGGCTGGCAGCCTCGGCGCTTTGTTTTTCACTACTACGAC	375
QY	301	TCTCAATCTGCTCAAGACACATTTCTCAATGGAAGAAAGATTAGGAATACGTC	360
DB	376	TCTCAATCTGCTCAAGACACATTTCTCAATGGAAGAAAGATTAGGAATACGTC	435
QY	361	RAGAGTTCGAATCTTCAAGTCCAGATATAGCTTGCAGGAGTCTGCAGATGCG	420
DB	436	RAGAGTTCGAATCTTCAAGTCCAGATATAGCTTGCAGGAGTCTGCAGATGCG	495
QY	421	CTGAAAACTCTGCTGAGCTGTATACAAAGCTGGAGCACACAGGTGCGCCCTGTA	480
DB	496	CTGAAAACTCTGCTGAGCTGTATACAAAGCTGGAGCACACAGGTGCGCCCTGTA	555
QY	481	CAGAACTGGAATGGCATGGAGCAATTTGCTACAGTTCTATAAAGACAGCAAAAGT	540
DB	556	CAGAACTGGAATGGCATGGAGCAATTTGCTACAGTTCTATAAAGACAGCAAAAGT	615
QY	541	GGGAGACTGTAATATTCTGCTTGTGAACTCTACCATGCTGAGGATGAAACAAAC	600
DB	616	GGGAGACTGTAATATTCTGCTTGTGAACTCTACCATGCTGAGGATGAAACAAAC	675
QY	601	AAGAGACTGGAATTTGCGCGCTCTCAGAGTCTCTGAGTTTCTACTCTTATGGA	660
DB	676	AAGAGACTGGAATTTGCGCGCTCTCAGAGTCTCTGAGTTTCTACTCTTATGGA	735
QY	661	CAGGCTTTTGGCGCTGACAGTGGCAAGCCTGGCTGTGGATGATGGAACCCCTTCA	720
DB	736	CAGGCTTTTGGCGCTGACAGTGGCAAGCCTGGCTGTGGATGATGGAACCCCTTCA	795
QY	721	CTTCTGAATGTTTCCATATATATATAGATGTCACAGCCCAAGAGCAGAGCTGTGG	780
DB	796	CTTCTGAATGTTTCCATATATATATAGATGTCACAGCCCAAGAGCAGAGCTGTGG	855
QY	781	CCATCTTAATGGGATGATCTCTCAAGGACTGCAAGAGATTGAGCGTTGTGCTGTG	840
DB	856	CCATCTTAATGGGATGATCTCTCAAGGACTGCAAGAGATTGAGCGTTGTGCTGTG	915

QY	841	AGAGAAGGCGAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAAACATTAGCG	900
DB	916	AGAGAAGGCGAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAAACATTAGCG	975
QY	901	AAGGTGACTGATTCCGCCCTCTGCAACTACAATAGCAGAGTGCAGCGGTGCCAAG	960
DB	976	AAGGTGACTGATTCCGCCCTCTGCAACTACAATAGCAGAGTGCAGCGGTGCCAAG	1035
QY	961	CAAGGCTAGTTGAGACATTTGGAAATGGAACATAATCAGGAAAGCATCTCTCTGACT	1020
DB	1036	CAAGGCTAGTTGAGACATTTGGAAATGGAACATAATCAGGAAAGCATCTCTCTGACT	1095
QY	1021	AGTACAAAATGGGTTCTCGTGTTCCTGTTGAGGATCACCAGCATTTCTGAGCTTGGGT	1080
DB	1096	AGTACAAAATGGGTTCTCGTGTTCCTGTTGAGGATCACCAGCATTTCTGAGCTTGGGT	1155
QY	1081	TATGACAGCTATTTAACAGTCAAGAACTCTTTATTATGATGCCCAACCAACCTCAGAA	1140
DB	1156	TATGACAGCTATTTAACAGTCAAGAACTCTTTATTATGATGCCCAACCAACCTCAGAA	1215
QY	1141	ACCCATAATGTCATCTGCTTCTTGGCTTAGAGATAACTTTTAGCTCTCTTTCTCAA	1200
DB	1216	ACCCATAATGTCATCTGCTTCTTGGCTTAGAGATAACTTTTAGCTCTCTTTCTCAA	1275
QY	1201	TGTCATAATCACCCTCCCTGTTTTCATGCTCTTCTTACACTTGTGGAAATAGAACTTT	1260
DB	1276	TGTCATAATCACCCTCCCTGTTTTCATGCTCTTCTTACACTTGTGGAAATAGAACTTT	1335
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DB	1336	TTGAGTAGAGGAATATACATTGAGTAACATCTTCTCTGACAGTCAAGTAGTCCATC	1395
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DB	1456	GTTTCAGTTTCATATAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCTTGTCA	1515
QY	1441	TGCGGTTTCCCAAGGAGTGTCACTTGTATGAGAAATCTCAATCTCAATGCTTATAA	1500
DB	1516	TGCGGTTTCCCAAGGAGTGTCACTTGTATGAGAAATCTCAATCTCAATGCTTATAA	1575
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DB	1576	GCAATCTCTCTGTGTCATTAAGACTCTGATAATTTGCTCCCTCCATAGGAATTTCTC	1635
QY	1561	CCAGAAAGAAATATATCCCATCTCCGTTTTCATATCAGAACTACCGTCCCGATTTCC	1620
DB	1636	CCAGAAAGAAATATATCCCATCTCCGTTTTCATATCAGAACTACCGTCCCGATTTCC	1695
QY	1621	CTTCAGAGAGATTAAAGACCAAGAAAGTGCAGCTCTTCACTGCACCTGTAAATGTT	1680
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QY	1681	CAGTTCCTTATTTTCTTCCATTGACCATATTTATACCTTTCCAGGTACTGAAATTAATA	1740
DB	1756	CAGTTCCTTATTTTCTTCCATTGACCATATTTATACCTTTCCAGGTACTGAAATTAATA	1815
QY	1741	ATAATAATGTAAATATCTGTGAAAAA	1766
DB	1816	ATAATAATGTAAATATCTGTGAAAAA	1841

RESULT 14
US-09-992-598-318
; Sequence 318, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          99.3%; Score 1764.4; DB 9; Length 1841;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTCACAGTAGCCCGGGCCCGCCAGGCGCAATCCGACCAATTTCACTCTCACCCTGTAG 60
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DB 136 GAATCCAGATGACGCGCAAGTACAGCAGCAGGAGGACATGCTGGATGATGATGGGACA 195
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DB 196 CCACCATGAGCTGCAATTTCTCAAGCCTCTGCGACAACTCGGCATCCAGAGCCCGCGCA 255
QY 181 CAGAGCAGAGGCTCCCTTTCAAGCTGGCGGACAGTGGCCCTGACCCCTGCTGACTTGT 240
DB 256 CAGAGCAGAGGCTCCCTTTCAAGCTGGCGGACAGTGGCCCTGACCCCTGCTGACTTGT 315
QY 241 GCTTGGTCTGCTGATAGGCTGGCAGCCCTGGGGCTTTTGTGTTTTTTCAGTACTACGAGC 300
DB 316 GCTTGGTCTGCTGATAGGCTGGCAGCCCTGGGGCTTTTGTGTTTTTTCAGTACTACGAGC 375

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361 AAGAGTTGCAATCTCTTCAAGTCCAGATATAAAGCTTGCAGGAGTCTGCAGCATGTGG 420
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QY 1381 GTTTCAGTTTCATCTAGTCCCTCCCAATCCATCAGTAAAGACCCCATCTCGCTTGTCGA 1440
Db 1456 GTTTCAGTTTCATCTAGTCCCTCCCAATCCATCAGTAAAGACCCCATCTCGCTTGTCGA 1515
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QY 1741 ATAATAAATGAAATACGTGAAAAA 1766
Db 1816 ATAATAAATGAAATACGTGAAAAA 1841

RESULT 15

US-09-989-293A-318
; Sequence 318, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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; PRIOR APPLICATION NUMBER: 60/075945
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; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
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; PRIOR APPLICATION NUMBER: 60/087106
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.3%; Score 1764.4; DB 9; Length 1841;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTCACAGTAGCCCGGGGGCCAGGGCAATCCGACCACTTCTCACTCTCACCGCTGTAG 60

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QY 121 CCACATGAGCCTGCAATTCCTCAAGCCTCTGCGCACTGCGGATCCAGAGCCCGGCGCA 180

Db 196 CCACATGAGCCTGCAATTCCTCAAGCCTCTGCGCACTGCGGATCCAGAGCCCGGCGCA 255

QY 181 CAGAGCAGGCGTCCCTCTTCAAGTGGCGACAGTGGCCCTGACCTGCTGACTTTGT 240

Db 256 CAGAGCAGGCGTCCCTCTTCAAGTGGCGACAGTGGCCCTGACCTGCTGACTTTGT 315

QY 241 GCTTGGTCTGCTGATAGGGCTGGCAGGCCCTGGGGCTTTTGTCTTTCAGTACTACCAGC 300

Db 316 GCTTGGTCTGCTGATAGGGCTGGCAGGCCCTGGGGCTTTTGTCTTTCAGTACTACCAGC 375

QY 301 TCTCCAATGCTGGTCAAGACACCAATTTCTCAATGGAAGAAAGATTAGAAATAGTCCC 360

Db 376 TCTCCAATGCTGGTCAAGACACCAATTTCTCAATGGAAGAAAGATTAGAAATAGTCCC 435

QY 361 AAGAGTTGCAATCTTCAAGTCCAGATATAAAGCTTTCAGGAAGTCTGCAGCATGTGG 420

Db 436 AAGAGTTGCAATCTTCAAGTCCAGATATAAAGCTTTCAGGAAGTCTGCAGCATGTGG 495

QY 421 CTGAAAACTCTGTGCTGAGCTGTATACAAAGCTGGAGACACACAGGTGCAGCCCTTGA 480

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QY 481 CAGAACAAATGGAAATGGCATGGAGACAAATGCTACCACTTCTATAAAGACAGCAAAAGTT 540

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QY 541 GGGAGGACTGTAAATATTTCTGCCCTTAGTGAAGAACTCTACCATGCTGAAGATAACAAC 600

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QY 601 AAGAGACTTGAATTTGCGCGCTCTCAGAGTACTCTGAGTTTTTCTACTCTTATTGA 660

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QY 661 CAGGGCTTTTGGCCCTGACAGTGGCAAGGCTGGCTGTGGATGGATGGAAACCCCTTTCA 720

Db 736 CAGGGCTTTTGGCCCTGACAGTGGCAAGGCTGGCTGTGGATGGATGGAAACCCCTTTCA 795

QY 721 CTTCTGAGCTTCCATATTTATATAGTGTCCAGCCCAAGAGAGCAGACACTGTGTGG 780

Db 796 CTTCTGAGCTTCCATATTTATATAGTGTCCAGCCCAAGAGAGCAGACACTGTGTGG 855

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Search completed: October 8, 2005, 00:59:08
Job time : 1188 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 19:46:51 ; Search time 5317 Seconds
(without alignments)
12714.339 Million cell updates/sec

Title: US-10-689-742-159

Perfect score: 1776
Sequence: 1 agctcacagtgcgcggcg...ctgtgaaaaa... 1776

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1732.4	97.5	1734	CR591145	CR591145 full-length
2	1690.4	95.2	1692	CR591231	CR591231 full-length
3	1671.4	94.1	1673	CR606141	CR606141 full-length
4	1669.4	94.0	1671	CR614400	CR614400 full-length
5	1651.4	93.0	1747	CR619172	CR619172 full-length
6	1554	87.5	1759	CR598502	CR598502 full-length
7	1027.6	57.9	1045	CR599905	CR599905 full-length
8	1001.4	56.4	1003	CR604680	CR604680 full-length
9	998.4	56.2	1068	CR599904	CR599904 full-length
10	966.6	54.4	1076	CR380211	CR380211 full-length
11	912.4	51.4	990	CR339074	CR339074 full-length
12	912.2	51.4	996	CR358356	CR358356 full-length
13	907.2	51.1	1049	AL541315	AL541315 full-length
14	865.4	48.7	914	CR391810	CR391810 full-length
15	855	48.1	1001	CR324788	CR324788 full-length
16	846.4	47.7	958	CR399696	CR399696 full-length
17	845.8	47.6	998	AL568840	AL568840 full-length
18	812.4	45.7	927	CR358357	CR358357 full-length
19	808.2	45.5	919	BQ722745	BQ722745 full-length
20	807.2	45.5	1078	BM920364	BM920364 full-length
21	806.4	45.4	1076	CR337172	CR337172 full-length
22	805.8	45.4	860	CR373476	CR373476 full-length
23	797	44.3	834	CR380078	CR380078 full-length
24	786.2	44.3	971	CR399695	CR399695 full-length

25	776.6	43.7	964	5	CR591145	1734 bp	linear	HTC 21-JUL-2004
26	768.4	43.3	770	5	CR591145	full-length cDNA clone	CSOD1049YB09 of Placenta Cot 25-normalized	
27	750.2	42.2	964	5	CR591145	of Homo sapiens (human).		
28	741.2	41.7	912	5	CR591145	HTC; CDSLT cDNA.		
29	729.4	41.1	732	5	CR591145	Homo sapiens (human)		
30	722	40.7	830	4	CR591145	Homo sapiens		
31	719.2	40.5	866	5	CR591145	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
32	706.2	39.8	1042	5	CR591145	Li.W.B., Gruber, C., Jessee, J. and Polayes, D.		
33	678.4	38.2	801	7	CR591145	Full-length cDNA libraries and normalization		
34	664.2	37.4	875	7	CR591145	Unpublished		
35	645.2	36.3	913	5	CR591145	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue		
36	631.8	35.6	832	6	CR591145	Genoscope.		
37	627.4	35.3	819	6	CR591145	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)		
38	619.2	34.9	941	4	CR591145	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of invitrogen.		
39	574	32.3	574	4	CR591145	Location/Qualifiers		
40	572.4	32.2	3084	3	CR591145	1. 1734		
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45	523	29.4	690	5	CR591145	/tissue type="Placenta Cot 25-normalized"		
					CR591145	/plasmid="pCMVSPORT_6"		

ALIGNMENTS

RESULT 1	CR591145	1734 bp	linear	HTC 21-JUL-2004
LOCUS	CR591145	full-length cDNA clone	CSOD1049YB09 of Placenta Cot 25-normalized	
DEFINITION	CR591145	of Homo sapiens (human).		
ACCESSION	CR591145	HTC; CDSLT cDNA.		
VERSION	CR591145.1	GI:50471952		
KEYWORDS	HTC; CDSLT cDNA.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	1 (bases 1 to 1734)			
AUTHORS	Li.W.B., Gruber, C., Jessee, J. and Polayes, D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished			
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue			
REFERENCE	2 (bases 1 to 1734)			
AUTHORS	Genoscope.			
TITLE	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :			
JOURNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)			

COMMENT
- Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of invitrogen.

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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ORIGIN

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1733; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 25 GGGCAATCCGACCATTTTCACTCTCCCGCTGTAGGAATCCAGATGCAGGCAAGTACA 84
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Db 1 GGGCAATCCGACCATTTTCACTCTCCCGCTGTAGGAATCCAGATGCAGGCAAGTACA 60

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QY	145	CCTCTGCCACAACCTGGGCATCCAGAGCCCGGGCGCAGAGCACAGGGCTCCCTCTTCAA	204
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QY	121	GCTCTGCCACAACCTGGGCATCCAGAGCCCGGGCGCAGAGCACAGGGCTCCCTCTTCAA	180
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QY	205	CGTGGCAGCAGTGGCCCTGACCTCTGCTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGG	264
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QY	181	CGTGGCAGCAGTGGCCCTGACCTCTGCTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGG	240
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QY	265	CAGCCCTGGGGCTTTTGTGTTTTTTCAGTACTACAGCTCTCCAACTACTGGTCAAGACCA	324
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QY	241	CAGCCCTGGGGCTTTTGTGTTTTTTCAGTACTACAGCTCTCCAACTACTGGTCAAGACCA	300
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QY	325	TTTCTCAAAATCGAAGAAAGATTAGAAATAGCTGCCAAGAGTTGCCAATCTCTTCAAGTCC	384
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QY	301	TTTCTCAAAATCGAAGAAAGATTAGAAATAGCTGCCAAGAGTTGCCAATCTCTTCAAGTCC	360
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QY	385	AGAAATAAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAACTCTGTCGTGAGCTGT	444
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QY	361	AGAAATAAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAACTCTGTCGTGAGCTGT	420
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QY	445	ATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACTAGAAATGGCATGGAG	504
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QY	481	ACAATTTGCTACAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAATATATTTCTGCC	540
DB			
QY	565	TTAGTGAAGACTCTACCATGCTGAAGATAAACAAAGAGAGCCTCGAAATTTGCGCGCT	624
DB			
QY	541	TTAGTGAAGACTCTACCATGCTGAAGATAAACAAAGAGAGCCTCGAAATTTGCGCGCT	600
DB			
QY	625	CTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGCAGGGCTTTTGGCGCCCTGCACAGTG	684
DB			
QY	601	CTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGCAGGGCTTTTGGCGCCCTGCACAGTG	660
DB			
QY	685	GCAAGGCTTGCTGTGATGATGGAACCCCTTTTCACTTCTGAACTGTTCCATATATATAA	744
DB			
QY	661	GCAAGGCTTGCTGTGATGATGGAACCCCTTTTCACTTCTGAACTGTTCCATATATATAA	720
DB			
QY	745	TAGATGTCACAGCCCAAGAGCAGAGACTGTGTGGCCATCTTAATGGGATGATCTTCT	804
DB			
QY	721	TAGATGTCACAGCCCAAGAGCAGAGACTGTGTGGCCATCTTAAATGGGATGATCTTCT	780
DB			
QY	805	CAAAAGGACTGCAAAAGATTGAAGCGTTGTGCTGTGAGAGAAGGCGCAGGAATGGTGAAGC	864
DB			
QY	781	CAAAAGGACTGCAAAAGATTGAAGCGTTGTGCTGTGAGAGAAGGCGCAGGAATGGTGAAGC	840
DB			
QY	865	CAGAGGCTCCATGTCCCCCTGAAAATTTAGGCGAAGGTGACTGATTCGCCCTCTGCA	924
DB			
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DB			
QY	925	ACTACAAATAGCAGAGTGAGCCAGCGGTGCAAAAGCAAGGCTAGTTGAGACATTTGGGA	984
DB			
QY	901	ACTACAAATAGCAGAGTGAGCCAGCGGTGCAAAAGCAAGGCTAGTTGAGACATTTGGGA	960
DB			
QY	985	AATGGACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAATGGGTTCTCGTGTTTT	1044
DB			
QY	961	AATGGACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAATGGGTTCTCGTGTTTT	1020
DB			
QY	1045	CCTGTTCAGGATCACCGACATTTCTGAGCTTTGGGTTTTATGCAGCTATTTAAACAGTCAAA	1104
DB			
QY	1021	CCTGTTCAGGATCACCGACATTTCTGAGCTTTGGGTTTTATGCAGCTATTTAAACAGTCAAA	1080
DB			
QY	1105	GAAGTCTTATTTACATGCCAACCAACCTCAGAAAACCCANATATGCTATCTGCTTCTTT	1164
DB			
QY	1081	GAAGTCTTATTTACATGCCAACCAACCTCAGAAAACCCATATATGCTATCTGCTTCTTT	1140
DB			

RESULT 2	CR591231	1692 bp	mrna	linear	HTC 21-JUL-2004
LOCUS	CR591231				
DEFINITION	full-length cDNA clone CS0DI041YA14 of Placentia Cot 25-normalized of Homo sapiens (human).				
ACCESSION	CR591231				
VERSION	CR591231.1	GI:50472038			
KEYWORDS	HTC; CNSLT_cDNA..				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paraday Avenue 2 (bases 1 to 1692) Genoscope.				
REFERENCE	Genoscope.				
AUTHORS	Direct Submission				
TITLE	Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage :				
JOURNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrsf@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime ends enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.				
FEATURES	Location/Qualifiers				
source	1..1692				

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Query Match 95.2%; Score 1690.4; DB 3; Length 1692;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1691; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 85 GCAGCAGGAGGACATCTGGATGATGATGGGACACACCATGAGCCTGCAATCTCAAG 144
DB 61 GCAGCAGGAGGACATCTGGATGATGATGGGACACACCATGAGCCTGCAATCTCAAG 120
QY 145 CTTCTGCCCAACTCTGGCAATCCAGAGCCCGGCGCACAGACACAGGGCTCCCTCTTCAA 204
DB 121 GCTCTGCCCAACTCTGGCAATCCAGAGCCCGGCGCACAGACACAGGGCTCCCTCTTCAA 180
QY 205 CGTGGCGACAGTGGCCCTGACCTGCTGACTTGTGCTTGTGCTGCTGATAGGCTGG 264
DB 181 CGTGGCGACAGTGGCCCTGACCTGCTGACTTGTGCTTGTGCTGCTGATAGGCTGG 240
QY 265 CAGCCCTGGGGCTTTTGTGTTTTTTCAGTACTACAGCTCTCCAACTACTGCTCAAGCACCA 324
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QY 325 TTTCTCAATGGAAGAAATAGGAATACTGTCCTCAAGTGGTGGTGGTGGTGGTGGTGGTGG 384
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QY 385 AGAATAAAGCTTGCAGGAAGTCTGACATGCTGCAATGCTGCAATGCTGCAATGCTGCAAT 444
DB 361 AGAATAAAGCTTGCAGGAAGTCTGACATGCTGCAATGCTGCAATGCTGCAATGCTGCAAT 420
QY 445 ATAAACAAGCTGAGCACACAGTGCAGCCCTTTGTACAGAACTATGGAATGGCATGGAG 504
DB 421 ATAAACAAGCTGAGCACACAGTGCAGCCCTTTGTACAGAACTATGGAATGGCATGGAG 480
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QY 565 TTAGTGAATACTCTACCATGCTGAGATATAACAACAAGACCTGGAATTTGGCGGT 624
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DB 781 CAAAGGACTGCAAGAAATGAAAGCTGTGTGAGAGAGGCGGCAAGGATGGTGAAGC 840
QY 865 CAGAGAGCTTCCATGTCCTCCCTTGAACCAATAGGCGAAGGTGACTGATTCGCGCTTGA 924
DB 841 CAGAGAGCTTCCATGTCCTCCCTTGAACCAATAGGCGAAGGTGACTGATTCGCGCTTGA 900
QY 925 ACTACAAATAGCAGAGTGAAGCGGCTGCGCAAGGCGGTAGTTGAGACATTTGGGA 984

DB 901 ACTACAAATAGCAGAGTAGCCAGCGGTGCCAAGCAAGGCTAGTTGAGACATTTGGGA 960
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QY 1705 CCATATTTTATAC 1716
DB 1681 CCATATTTTATAC 1692

RESULT 3

CR606141

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

full-length cDNA clone CS0DE006YK19 of Placenta of Homo sapiens
(human).
CR606141
CR606141.1 GI:50486948
HTC; CNSLT cdna.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1673)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1.1673
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FEATURES
source

ORIGIN
Query Match 94.1%; Score 1671.4; DB 3; Length 1673;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 77 CAAGTACAGCAGCAGGAGCATGCTGATGATGATGGGACACCCACCATGAGCTGCA 136
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QY 137 TTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCGGGCCACAGAGCAGAGGGCTCC 196
Db 61 TTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCGGGCCACAGAGCAGAGGGCTCC 120

QY 197 CTCCTCAAGCTGGCAGCAGTGGCCCTGACCTGCTGACTTTGCTTGGTGGTGGTGGT 256
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QY 257 AGGGCTGGCAGCCTGGGGCTTTCTTTTTCAGTACTACAGCTCTCCAACTACTGGTCA 316
Db 181 AGGGCTGGCAGCCTGGGGCTTTCTTTTTCAGTACTACAGCTCTCCAACTACTGGTCA 240

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QY 377 TCAAGTCCAGAAATATAAAGCTTGAGGAAGTCTGCAGCATGTCGAGCAATGTCGTCG 436
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QY 437 TGAGCTGTATACAAAGCTGGAGCACACAGGTGACGCTTGTACAGAACCAATGGAAATG 496
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QY 497 GCATGGAGACAATTTGCTACCAAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAATA 556
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QY 977 CATTGGGAAATGGAACATAATCAGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTTC 1036
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RESULT 4
CR614400
LOCUS
DEFINITION full-length cDNA clone CS0DI036YF20 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR614400


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VERSION CR614400.1 GI:50495207
KEYWORDS HTC; CNSLT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
REMARK Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1671)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1670; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 841 GAAGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGAAGCCAGGGGCTGCCAAA 900
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DB 1141 ATGTCATAATCATCCTCCCTGTTTCTGCTTCTTCTTACCTGGTGAATAAGAACTT 1200
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QY 1560 CCGAGGAAGAAATATATCCCATCTCGTTTTCATATCAGAACTACCGTCCCCCATATTC 1619
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QY 1680 TCAGTTCCTATTCTTCATGACCCCATATTATATACCTTTCAGGTACTGA 1730
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Db 1621 TCAGTTCCTATTCTTCATGACCCCATATTATATACCTTTCAGGTACTGA 1671

RESULT 5
CR619172 1747 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DI067YK14 of Placentia Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR619172
VERSION CR619172.1 GI:50499979
KEYWORDS HTC; CNSLT cdna.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1747)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
REFERENCE 2 (bases 1 to 1747)
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of invitrogen.
FEATURES
source
Location/Qualifiers
1..1747
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI067YK14"
/tissue_type="Placentia Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
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Best Local Similarity 97.5%; Pred. No. 0;
Matches 1704; Conservative 0; Mismatches 1; Indels 42; Gaps 1;

QY 30 ATCCGACCACATTTTCACTCTCACCGCTGTAGGAATCCAGATGCGGCCCAAGTACAGCAGC 89
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Db 1 ATCCGACCACATTTTCACTCTCACCGCTGTAGGAATCCAGATGCGGCCCAAGTACAGCAGC 60
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QY 90 ACGAGGAGATGCTGGATGATGATGGGACACACCATGAGCTGCATTCACAGCCCTCT 149
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Db 61 ACGAGGAGATGCTGGATGATGATGGGACACACCATGAGCTGCATTCACAGCCCTCT 120
|||||

QY 150 GCCCAACTCCGCATCCAGAGCCCGCGGCACAGAGCAGGGCTCCCTCTTCAACGTGG 209
|||||
Db 121 GCCCAACTCCGCATCCAGAGCCCGCGGCACAGAGCAGGGCTCCCTCTTCAACGTGG 180
|||||

QY 210 CGACCAGTGGCCCTGACCTGCTGACTTGTGCTTGGTGTGCTGATAGGGCTGCGAGCC 269
|||||
Db 181 CGACCAGTGGCCCTGACCTGCTGACTTGTGCTTGGTGTGCTGATAGGGCTGCGAGCC 240
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QY 270 CTGGGGCTTTTGT-----TTTTT 287
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Db 241 CTGGGGCTTTTGTGTAAGTCTGCGCTCTGACCTGGGGGAGGATCCTGGTTCCAAAGTTTTT 300
|||||

QY 288 CAGTACTACAGCTCTCCAATACTCGTCAAGACACCATTTCTCAATGGAAGAAGATTA 347
|||||
Db 301 CAGTACTACAGCTCTCCAATACTCGTCAAGACACCATTTCTCAATGGAAGAAGATTA 360
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QY 348 GGAATACGTCCTCCAGAGTTGCAATCTCTTCAAGTCCAGAAATATAAAGCTTGCAGGAAGT 407
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Db 361 GGAATACGTCCTCCAGAGTTGCAATCTCTTCAAGTCCAGAAATATAAAGCTTGCAGGAAGT 420
|||||

QY 408 CTGAGCATGTGGCTGAAAACTCTGCTGAGCTGTATACAAAGCTGGAGGCACACAGG 467
|||||
Db 421 CTGAGCATGTGGCTGAAAACTCTGCTGAGCTGTATACAAAGCTGGAGGCACACAGG 480
|||||

QY 468 TGCAGCCCTTGTACAGAAACAATGGAATGGCATGGAGACAATTGCTACAGTCTTATAAA 527
|||||
Db 481 TGCAGCCCTTGTACAGAAACAATGGAATGGCATGGAGACAATTGCTACAGTCTTATAAA 540
|||||

QY 528 GACAGCAAAAGTGGAGGACTGTAAATATTCTTGCCTTACTGAAAACTTACCATGTG 587
|||||
Db 541 GACAGCAAAAGTGGAGGACTGTAAATATTCTTGCCTTACTGAAAACTTACCATGTG 600
|||||

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Db 601 AAGATAACAACAAGAGAGACTGGAAATTTGCCGCTCTCAGAGTACTCTGAGTTTTTC 660
|||||

QY 648 TACTCTTATTGGACAGGGCTTTTGGCCCTGACAGTGGCAAGGCTGCTGTGATGAT 707
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Db 661 TACTCTTATTGGACAGGGCTTTTGGCCCTGACAGTGGCAAGGCTGCTGTGATGAT 720
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QY 708 GGAACCCCTTTCACTCTGAACTGTTCATATTATATATAGATGTACAGCCCAAGAAAGC 767
|||||
Db 721 GGAACCCCTTTCACTCTGAACTGTTCATATTATATATAGATGTACAGCCCAAGAAAGC 780
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QY 768 AGAGACTGTGGCCATCCTTAATGGGATGATCTTCAAAAGGACTGCAAAAGATTGAAG 827
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QY 828 CGTTGTGCTCTGAGAGAAGGGCAGGAATGTAAGCCAGAGAGCCTCCATGTCCCCCT 887
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Db 841 CGTTGTGCTCTGAGAGAAGGGCAGGAATGTAAGCCAGAGAGCCTCCATGTCCCCCT 900
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QY 888 GAAACATTAGCGAAGGTGACTGATTCGCCCTCTGCAACTCAAAATAGCAGAGTGAGCCA 947
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Db 1021 TATCTCTGACTAGTACAAAATGGGTTCTCGTGTCTTCTGCTTCCAGGATCACAGCATTT 1080
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QY 1068 CTGAGCTTGGGTTTATGCACTGATTTTAACTCAAGAGTCTTTATTTATGCGCACCA 1127
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Db 1081 CTGAGCTTGGGTTTATGCACTGATTTTAACTCAAGAGTCTTTATTTATGCGCACCA 1140
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QY 1128 ACCAACCTCAGAAACCCATATATGTCATGCTTCTTGGCTTTAGAGATAAATTTTGTGCTC 1187
|||||
Db 1141 ACCAACCTCAGAAACCCATATATGTCATGCTTCTTGGCTTTAGAGATAAATTTTGTGCTC 1200
|||||

QY 1188 TCTTTCTCTCAATGTCTTAATATCACTCCCTGTTTTCATGTCTTCTTACACTTGGTGG 1247
|||||
Db 1201 TCTTTCTCTCAATGTCTTAATATCACTCCCTGTTTTCATGTCTTCTTACACTTGGTGG 1260
|||||

QY 1248 AATAAGAAATTTTGAAGTAGAGAAATAATTGAGGTAAATCATCTTTTCTCTGACAGT 1307
|||||
Db 1261 AATAAGAAATTTTGAAGTAGAGAAATAATTGAGGTAAATCATCTTTTCTCTGACAGT 1320
|||||

QY 1308 CAAGTAGTCCATCAGAAATTTGGCAGTCACTTCCAGATTGTACCAGCAAAATACACAAGA 1367
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Db 1321 CAAGTAGTCCATCAGAAATTTGGCAGTCACTTCCAGATTGTACCAGCAAAATACACAAGA 1380
|||||

QY 1368 ATTCTTTTGTGTTTGTTCAGTTCATCTAGTTCCTTCCCAATCCATCAGTAAAGACCCCA 1427
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QY 1428 TCTGCTTGTCTCATGCGCGTTTCCCAACAGGGATGTCACTTGTATGAGAAATCTCAATCT 1487
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Db 1441 TCTGCTTGTTCATGCGGTTTCCCAACAGGAGTGTCACTTGATATGAGAAATCTCAAAATCT 1500
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Db 1501 CAATGCTTTATAGCAATTCCTTCTGTGTGCCATTAGACTCTGATAATTTGTCTCCCTCC 1560
Qy 1548 ATAGGAATTTCTCCAGGAAGAAATATATATCCCATCTCCGTTTCAATATCAGAACTACCG 1607
Db 1561 ATAGGAATTTCTCCAGGAAGAAATATATATCCCATCTCCGTTTCAATATCAGAACTACCG 1620
Qy 1608 TCCCGCATATTCCTTCCAGAGATTAAGAGACAGAGAAAGAGTGTGAGCTCTTCACTGCA 1667
Db 1621 TCCCGCATATTCCTTCCAGAGATTAAGAGACAGAGAAAGAGTGTGAGCTCTTCACTGCA 1680
Qy 1668 CTGTAATAGTTTCAAGTTCCTATTTTCTTCCATTTGACCCATATTTATACCTTTTCAGGTAC 1727
Db 1681 CCGTAATAGTTTCAAGTTCCTATTTTCTTCCATTTGACCCATATTTATACCTTTTCAGGTAC 1740
Qy 1728 TGAAGAT 1734
Db 1741 TGAAGAT 1747

RESULT 6
CRS98502
LOCUS full-length cDNA clone CS0D1044YF02 of Placentia Cot 25-normalized
DEFINITION full-length cDNA clone CS0D1044YF02 of Placentia Cot 25-normalized
ACCESSION CRS98502
VERSION CRS98502.1 GI:50479309
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
JOURNAL Full-length cDNA libraries and normalization
REMARK Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
1..1759
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1044YF02"
/tissue_type="Placentia Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Query Match 87.5%; Score 1554; DB 3; Length 1759;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1561; Conservative 0; Mismatches 25; Indels 2; Gaps 1;
Qy 124 CCATGAGCTGATTTCTCAAGCTCTGCCACAACCTCGGCATCCAGAGCCCGGCCG--CAC 181
Db 152 CTTTGACCTCCCTGGCTCAAGCAATCTCCACCTCAGCCTTCTGAGTAGCTGGCACTAC 211
Qy 182 AGAGCACAGGGTCCCTCTTCAACGTGGGACCAAGTGGCCCTGACCCCTGCTGACTTTGTG 241
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Db 212 AGAGCACAGGGTCCCTCTTCAACGTGGGACCAAGTGGCCCTGACCCCTGCTGACTTTGTG 271
Qy 242 CTTTGTGCTGTGATAGGGCTGGCAGCCCTGGGGCTTTTGTGTTTTTTCAGTACTACCAGCT 301
Db 272 CTTTGTGCTGTGATAGGGCTGGCAGCCCTGGGGCTTTTGTGTTTTTTCAGTACTACCAGCT 331
Qy 302 CTCCTAATCTGCTCAAGACACCAATTTCTCAATATGAAGAAAGATTAGGAATAACGTCCTCA 361
Db 332 CTCCTAATCTGCTCAAGACACCAATTTCTCAATATGAAGAAAGATTAGGAATAACGTCCTCA 391
Qy 362 AGAGTTGCAATCTCTTCAAGTCCAGATATTAAGCTTGCAGGAAGTCTCAGCATGTGGC 421
Db 392 AGAGTTGCAATCTCTTCAAGTCCAGATATTAAGCTTGCAGGAAGTCTCAGCATGTGGC 451
Qy 422 TGAATAAATCTCTGCTGAGCTGTATATAACAAAGCTGGAGCACACAGGTGAGCCCTTTGTAC 481
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Qy 482 AGAACATGGAAATGGCATGGAGACAAATTTGTAACAGTTCTATATAAGACAGCAAAAGTTG 541
Db 512 AGAACATGGAAATGGCATGGAGACAAATTTGTAACAGTTCTATATAAGACAGCAAAAGTTG 571
Qy 542 GGAGGACTGTAAATATTTCTGCTTTAGTGAATACTTACCATGCTGAAGATATAACAAACA 601
Db 572 GGAGGACTGTAAATATTTCTGCTTTAGTGAATACTTACCATGCTGAAGATATAACAAACA 631
Qy 602 AGAAGACCTGTAAATTTGCGGCTCTCAGAGCTACTCTCAGTTTTTCTACTCTTATTGGAC 661
Db 632 AGAAGACCTGTAAATTTGCGGCTCTCAGAGCTACTCTCAGTTTTTCTACTCTTATTGGAC 691
Qy 662 AGGGCTTTTGGCCCTGACAGTGGCAAGGCTGTGGATGGATGGAAACCCCTTTTAC 721
Db 692 AGGGCTTTTGGCCCTGACAGTGGCAAGGCTGTGGATGGATGGAAACCCCTTTTAC 751
Qy 722 TTCTGAACCTGTTCATATTAATAGATGTCCAGAGCCCAAGACAGAGACTGTGTGGC 781
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Qy 782 CATCCTTAATGGGATGATCTTCTCAAGGACTCGCAAGAAATTTGAAGCGTTGTGTCTGTA 841
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Qy 842 GAGAAGGCGAGAAATGGTGAAGCCAGAGAGCTCCATGTCCCTGCTGAAACAAATAGGCGA 901
Db 872 GAGAAGGCGAGAAATGGTGAAGCCAGAGAGCTCCATGTCCCTGCTGAAACAAATAGGCGA 931
Qy 902 AGGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGGCCAGCGGTGCCAAGC 961
Db 932 AGGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGGCCAGCGGTGCCAAGC 991
Qy 962 AAGGCTAGTTTGAGACATTTGGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTA 1021
Db 992 AAGGCTAGTTTGAGACATTTGGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTA 1051
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Db 1052 GTACAAAATGGGTTCTCGTGTTCCTGTTTCAGGATCACAGCATTTCTGAGCTGGGTTT 1111
Qy 1082 ATGACAGCTATTTAACAGTCAAGAGTCTTATTATATGATGCCACCAACCTCAGAAA 1141
Db 1112 ATGACAGCTATTTAACAGTCAAGAGTCTTATTATATGATGCCACCAACCTCAGAAA 1171
Qy 1142 CCCATAATGTCATCTGCTTCTTGGCTTAGAGATAAATCTTTTAGCTCTCTTTCTTCTCAAT 1201
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Db 1232 GTCTAATATACCTCCCTGTTTTTCATGTTCTTCTTACACTTGGTGGAAATAAGAACTTTT 1291
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Db 1292 TGAAGTAGAGAAATACATTGAGGTAAACATCCTTTTCTGTGACAGTCAAGTAGTCCATCA 1351
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Db 1352 GAAATTGGCAGTCACTTCCAGATGTACAGCAAAATACAAAGAAATCTTTTGTGTTG 1411
Qy 1382 TTTCAGTTTCATAGTCCCTCCCAATCCATCCATAGTAAAGACCCCATCTGCTTGTCCAT 1441
Db 1412 TTTCAGTTTCATAGTCCCTCCCAATCCATCCATAGTAAAGACCCCATCTGCTTGTCCAT 1471
Qy 1442 GCCGTTTCCCAACAGGGATGTCATCTGATATGAGATCTCAAAATCTCAATGCCATTATAAG 1501
Db 1472 GCCGTTTCCCAACAGGGATGTCATCTGATATGAGATCTCAAAATCTCAATGCCATTATAAG 1531
Qy 1502 CATTCCTTCTGTGTCCATTAAGACTCTGATAATTTGTCTCCCTCCATAGGAAATTTCTCC 1561
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Qy 1562 CAGGAAAGAAATATATCCCATCTCCGTTTCATATCAGAACTACCGTCCCGATATCC 1621
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Qy 1622 TTCAGAGAGATTAAGACAGCAAAAAAGTGAAGCTTTCATCTGACACCTGTAATAGTTTC 1681
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Qy 1682 AGTTCTTATTTCTTCCATTCAGCCCATATTTATATCTTTTTCAGGTACTG 1729
Db 1712 AGTTCTTATTTCTTCCATTCAGCCCATATTTATATCTTTTTCAGGTACTG 1759

RESULT 7
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LOCUS
DEFINITION BX379905 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSOD1041YA14 5-PRIME, mRNA sequence.
ACCESSION BX379905
VERSION BX379905.2 GI:46557568
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1045)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30439428.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6541.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOD1041BA07QPI&c=6541.r.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1041YA14"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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ORIGIN

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Query Match 57.9%; Score 1027.6; DB 5; Length 1045;
Best Local Similarity 98.9%; Pred. No. 4.4e-274;
Matches 1034; Conservative 10; Mismatches 1; Indels 1; Gaps 1;
Qy 25 GGGCAATCCGACCAATTTTCACTCTCACCGCTGTAGGAATCCAGATGACAGGCCCAAGTACA 84
Db 1 GGGCAATCCGACCAATTTTCACTCTCACCGCTGTAGGAATCCAGATGACAGGCCCAAGTACA 60
Qy 85 GCAGCAGAGGAGCATGCTGGATGATGATGGGACACCAACCATGAGCCTGCATTCTCAAG 144
Db 61 GCAGCAGAGGAGCATGCTGGATGATGATGGGACACCAACCATGAGCCTGCATTCTCAAG 120
Qy 145 CCTCTGCCACAATCCGGCATCCAGAGCCCCGGCGCACAGAGCACAGGGCTCCCTCTTCAA 204
Db 121 GCTCTGCCACAATCCGGCATCCAGAGCCCCGGCGCACAGAGCACAGGGCTCCCTCTTCAA 180
Qy 205 CGTGGCAGCAGTGGCCCTGACCCCTGTGACTTTGTGCTTGGTGTGCTGTGATAGGGCTGG 264
Db 181 CGTGGCAGCAGTGGCCCTGACCCCTGTGACTTTGTGCTTGGTGTGCTGTGATAGGGCTGG 240
Qy 265 CAGCCCTGGGGCTTTTGTGTTTTTTCAGTACTACAGCTCTCCAATCTGCTCAAGACACA 324
Db 241 CAGCCCTGGGGCTTTTGTGTTTTTTCAGTACTACAGCTCTCCAATCTGCTCAAGACACA 300
Qy 325 TTTCTCAAAATGGAAGAAATTTAGGAATACGTCCTCCAGAGTTGCAATCTCTTCAAGTCC 384
Db 301 TTTCTCAAAATGGAAGAAATTTAGGAATACGTCCTCCAGAGTTGCAATCTCTTCAAGTCC 360
Qy 385 AGAATATAAGCTTGCAGGAAAGTCTGACGATGTGGCTGGAAGAACTCTGTGCTGAGCTGT 444
Db 361 AGAATATAAGCTTGCAGGAAAGTCTGACGATGTGGCTGGAAGAACTCTGTGCTGAGCTGT 420
Qy 445 ATAACAAGCTGGAGCACACAGGTGACGCCCTGTACAGAAACAATGGAATGGCATGGAG 504
Db 421 ATAACAAGCTGGAGCACACAGGTGACGCCCTGTACAGAAACAATGGAATGGCATGGAG 480
Qy 505 ACAATTGCTACCACTTCTATTAAGACAGCAAAAAGTTGGAGGACTGTAAATATTTCTGCC 564
Db 481 ACAATTGCTACCACTTCTATTAAGACAGCAAAAAGTTGGAGGACTGTAAATATTTCTGCC 540
Qy 565 TTAGTGAATACTTACCATGCTGAAGATAACAACAAGAGAGAGCTGGAATTTGCCGGT 624
Db 541 TTAGTGAATACTTACCATGCTGAAGATAACAACAAGAGAGAGCTGGAATTTGCCGGT 600
Qy 625 CTCAGAGCTACTCTGAGTTTTTCTACTCTTATTTGACAGGGCTTTTGGCCCTGCACAGTG 684
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Qy 685 GCAAGGCTGCTGTGATGATGGAACCCCTTTTCACTTCTGAACCTGTTCCATATTATAA 744
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Qy 745 TAGATGTACAGCCCAAGAGAGAGACTGTGTGGCCATCCTTAATGGGATGATCTTCT 804
Db 721 TAGATGTACAGCCCAAGAGAGAGACTGTGTGGCCATCCTTAATGGGATGATCTTCT 780
Qy 805 CAAAGGCTGCAAGAATTGAAGCGTTGTGCTGTGAGAGAGGGCAGGAATGGTGAAGC 864
Db 781 CAAAGGCTGCAAGAATTGAAGCGTTGTGCTGTGAGAGAGGGCAGGAATGGTGAAGC 840
Qy 865 CAGAGAGCTCCATGTCCCCCTGAAAACATTTAGGCGAAGGTGACTGATTTCGCCCTCTGCA 924
Db 841 CAGAGAGCTCCATGTCCCCCTGAAAACATTTAGGCGAAGGTGACTGATTTCGCCCTCTGCA 900
Qy 925 ACTCAAAATAGCAGAGTGAGCCGGTGCACAAGCAAGGGCTAGTTGAGACATTTGGA 984
Db 901 ACTCAAAATAGCAGAGTGAGCCGGTGCACAAGCAAGGGCTAGTTGAGACATTTGGA 960
Qy 985 AATGGAACATTAATCAGGAAAGACTATCTCTGTAGTACTAGCAAAATGGTGTCTCTGTTT 1044
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QY 1045 CTTGTTCCAGATCACCAGCATTTCTG 1070
Db 1021 CTTGTTCCAGAT-MCCAGCATTTCTG 1045

RESULT 8
CR604680
LOCUS 1003 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0D1081YG24 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR604680
VERSION HTG; CNSLT cDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1003)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1003)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
1..1003
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1081YG24"
/tissue_type="placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

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Query Match 56.4%; Score 1001.4; DB 3; Length 1003;
Best Local Similarity 99.9%; Pred. No. 8.5e-267;
Matches 1002; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 CCCGGGGCCCGAGGCAATCCGACCAATTTCACTCTCACCGCTGTAGGAATCCAGATGC 72
Db 1 CCCGGGGCCCGAGGCAATCCGACCAATTTCACTCTCACCGCTGTAGGAATCCAGATGC 60

QY 73 AGGCCAAGTACAGCAGCAGGAGCATGCTGGATGATGATGGGACACACCATGAGGCC 132
Db 61 AGGCCAAGTACAGCAGCAGGAGCATGCTGGATGATGATGGGACACACCATGAGGCC 120

QY 133 TGCATTCTCAAGCTCTGCCAATCTGGCATCCAGAGCCCGCGGCACAGACACAGG 192
Db 121 TGCATTCTCAAGCTCTGCCAATCTGGCATCCAGAGCCCGCGGCACAGACACAGG 180

QY 193 CTCCTCTTCAACGTGGGACAGTGGCCCTGACCTGTGACTTTGTGTTGGTGTGCTGC 252
Db 181 CTCCTCTTCAACGTGGGACAGTGGCCCTGACCTGTGACTTTGTGTTGGTGTGCTGC 240

QY 253 TGATAGGCTGTCAGCCCTGGGGCTTTGTTTTTTCAGTACTACAGCTCTCCCAATCTG 312
Db 241 TGATAGGCTGTCAGCCCTGGGGCTTTGTTTTTTCAGTACTACAGCTCTCCCAATCTG 300

QY 313 GTCAGACACCAATTTCTCAATGGAGAAAGATTAGGAAATACGTCCCAAGAGTTGCAAT 372
Db 301 GTCAGACACCAATTTCTCAATGGAGAAAGATTAGGAAATACGTCCCAAGAGTTGCAAT 360

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For more information about this cluster, see

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373 CTCCTCAAGTCCAGAAATATAAGCTTCAGGAAGTCTGCAGCATGTGGTGAAACTCT 432
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433 GTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACATGGA 492
421 GTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACATGGA 480
493 AATGTCATGGAGACAAATTTGCTACCAAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTA 552
481 AATGTCATGGAGACAAATTTGCTACCAAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTA 540
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601 AATTGGCCGCTCTCAGAGCTACTCTGAGTTTTTTTCTACTCTTTATTTGGACAGGCTTTTTCG 660
673 GCCCTGACAGTGGCAAGCCCTGGCTGTGGATGGATGGAAACCCCTTTCTACTTCTGAACCTGT 732
661 GCCCTGACAGTGGCAAGCCCTGGCTGTGGATGGATGGAAACCCCTTTCTACTTCTGAACCTGT 720
733 TCCATATTTATATAGATGTCTACCAAGCCCAAGACAGAGACTGTGTGCGCCATCTTAATG 792
721 TCCATATTTATATAGATGTCTACCAAGCCCAAGACAGAGACTGTGTGCGCCATCTTAATG 780
793 GGATGATCTTCTCAAGGACTGCAAGAAATTTGAAGCGTTGTGTCTGTGAGAGAAGGGCAG 852
781 GGATGATCTTCTCAAGGACTGCAAGAAATTTGAAGCGTTGTGTCTGTGAGAGAAGGGCAG 840
853 GAATGGTGAAGCCAGAGAGCTTCCATGTCCTCCCTGAAACATTTAGCGAAGGTGACTGAT 912
841 GAATGGTGAAGCCAGAGAGCTTCCATGTCCTCCCTGAAACATTTAGCGAAGGTGACTGAT 900
913 TCGCCCTCTGCAACTACAAATAGCAGAGTGAGCAGGCGGTGCCAAACAGGCTAGTT 972
901 TCGCCCTCTGCAACTACAAATAGCAGAGTGAGCAGGCGGTGCCAAACAGGCTAGTT 960
973 GAGACATTTGGGAAATGGAACATAATACAGAAAGACTATCTCTC 1015
961 GAGACATTTGGGAAATGGAACATAATACAGAAAGACTATCTCTC 1003

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RESULT 9
BX379904/c

LOCUS BX379904 1068 bp mRNA linear EST 23-APR-2004
DEFINITION BX379904 Homo sapiens PLACENTA Cot 25-NORMALIZED Homo sapiens cDNA
clone CS0D1041YA14 3-PRIME, mRNA sequence.

ACCESSION BX379904
VERSION BX379904.2 GI:46555782
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1068)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 8, 2003 this sequence version replaced gi:30435570.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

6541.r

http://www.genoscope.cns.fr/cdna?s=CS0D1041BA07NP1&c=6541.r.
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue type="PLACENTA"
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/note="1st strand cDNA was primed with a NotI-oligo (dt)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 56.2%; Score 998.4; DB 5; Length 1068;
Best Local Similarity 99.0%; Pred. No. 5.9e-266;
Matches 1040; Conservative 5; Mismatches 1; Indels 4; Gaps 4;
Qy 668 TTTCGGCCCTGACAGTGGCAAGGCTGGCTGGATGATGGAACCCCTTTCACTTCGA 727
Db |||||
Qy 1047 TTTCGGCCCTGACAGT-GCAAGGCTGCTGTGGATGGATGG-ACCCCTTTTMACTTCGA 990
Db |||||
Qy 728 ACTGTTCCATTAATAATAGATGTACACAGCCCAAGAGACGAGACTGTGGCCATCCT 787
Db |||||
Qy 989 ACTGTTCCATTAATAATAGATGTACACAGCCCAAGAGACGAGACTGTGGCCATCCT 930
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Qy 788 TAATGGGATGATCTCTCAAGAGACTGCAAGAGATGGAAGCTGTGCTGTGAGAGAG 847
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Qy 929 TAATGGGATGATCTCTCAAGAGACTGCAAGAGATGGAAGCTGTGCTGTGAGAGAG 870
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Qy 848 GGCAGGAATGTGAAGCCAGAGAGCTCCATGTCCCTCCCTGAACATTAGCGGAAGTGA 907
Db |||||
Qy 869 GGCAGGAATGTGAAGCCAGAGAGCTCCATGTCCCTCCCTGAACATTAGCGGAAGTGA 810
Db |||||
Qy 908 CTGATTCGCCCTCTGCAACTACAAATAGCAGATGAGCCAGCGGTGCCAAGCAAGGCG 967
Db |||||
Qy 809 CTGATTCGCCCTCTGCAACTACAAATAGCAGATGAGCCAGCGGTGCCAAGCAAGGCG 750
Db |||||
Qy 968 TAGTTGACACATGCGAATCGAATACATAGCAGAGACTATCTCTGCTAGTACTAGTACA 1027
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Qy 749 TAGTTGACACATGCGAATCGAATACATAGCAGAGACTATCTCTGCTAGTACTAGTACA 690
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Qy 1028 AATGGTTCTCGTGTTCCTGTTCCAGGATCACCAGCATTTCTGAGCTGGGTTTATGCAC 1087
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Qy 689 AATGGTTCTCGTGTTCCTGTTCCAGGATCACCAGCATTTCTGAGCTGGGTTTATGCAC 630
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Qy 1088 GTATTTAACTGTCACAAAGATCTTATTTATCATGCCCAACCAACCTTCAGAAACCCCAT 1147
Db |||||
Qy 629 GTATTTAACTGTCACAAAGATCTTATTTATCATGCCCAACCAACCTTCAGAAACCCCAT 570
Db |||||
Qy 1148 ATGTCA-TCCTGCTTCTGGCTTAGAGATACTTTAGCTCTCTTCTTCTCAATGCTA 1206
Db |||||
Qy 569 ATGTCACCTCGCTTCTGGCTTAGAGATACTTTAGCTCTCTTCTTCTCAATGCTA 510
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Qy 1207 ATATCACCTCGCTTCTGCTCTCTTACACTTGGTGAATAAGAAACTTTTGAAG 1266
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Qy 509 ATATCACCTCGCTTCTGCTCTCTTACACTTGGTGAATAAGAAACTTTTGAAG 450
Db |||||
Qy 1267 TAGAGGAATAACATTTAGAGTAACTCTCTTCTCTGACAGTCAAGTAGTCCATCAGAAAT 1326
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Qy 449 TAGAGGAATAACATTTAGAGTAACTCTCTTCTCTGACAGTCAAGTAGTCCATCAGAAAT 390
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Qy 1327 TGGCAGTCACTTCCAGATTTGACCAAGATACACAGGAATCTTTTCTTCTTCTTCA 1386
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Db |||||
Qy 1387 GTTCATACCTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCCCTTGTCCATGCCGT 1446
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Qy 149 AAGAAATATATCCCATCTCCGTTTTCATATCAGAACTACCGTCCCGGATATTCCTTCAG 90
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Qy 1627 AGAGATTAAAGACAGAGAAAAGTGGAGCTCTTCATCTGCACCTGTATAGTTTCAGTTC 1686
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Qy 89 AGAGATTAAAGACAGAGAAAAGTGGAGCTCTTCATCTGCACCTGTATAGTTTCAGTTC 30
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Qy 1687 CTATTTCTTCCCATTTGACCCATATTTATAC 1716
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Qy 29 CTATTTCTTCCCA-TGACCCCATATTTATAC 1
Db |||||
RESULT 10
BX380211/c
LOCUS BX380211 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1044YF02 3-PRIME, mRNA sequence.
ACCESSION BX380211
VERSION BX380211.2 GI:46556700
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1076)
AUTHORS Li.W.B., Gruber.C., Jessee.J. and Polayes.D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 8, 2003 this sequence version replaced gi:30435625.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6541.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1044DC01NP1&c=6541.r.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1044YF02"
/tissue type="PLACENTA"
/clone.lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dt)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 54.4%; Score 966.6; DB 5; Length 1076;
Best Local Similarity 95.4%; Pred. No. 4.2e-257;
Matches 1006; Conservative 16; Mismatches 29; Indels 3; Gaps 3;
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Qy 1052 TGCCCTTAACAGGCGAGCGCKGTGGGDDGGAGMCCCTTMACTTCTGAAC-TTCCA 994
Db |||||
Qy 737 TATTATATAGATGTCTACCCAGCCCAAGAGAGAGACTGTGTGGCCATCCTTAATGGAT 796
Db |||||
Qy 993 TWTATATAGAT-TCAACAGCCCAAGAGAGAGACTKTGTGSCCATCTCTTAATGGAT 935
Db |||||

Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6541.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BAI029ZA09_CS02753_1&c=6541.r

FEATURES

source

Location/Qualifiers
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6
vector. Library was normalized."

ORIGIN

Query Match 48.7%; Score 865.4; DB 5; Length 914;
Best Local Similarity 99.2%; Pred. No. 5.7e-229;
Matches 869; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 157 CTCGCAATCCAGAGCCCGCGCAGAGACACAGGCTCCCTCTCAACGTGGCGACAG 216
DB 854 CTCGCAATCCAGAGCCCGCGCAGAGACACAGGCTCCCTCTCAACGTGGCGACAG 795

QY 217 TGGCCCTGACCCCTGCTGACTTTGTGCTGCTGATAGGGCTGGCAGCCCTCTGGGCG 276
DB 794 TGGCCCTGACCCCTGCTGACTTTGTGCTGCTGATAGGGCTGGCAGCCCTCTGGGCG 735

QY 277 TTTTGTGTTTTTTCAGTACACAGCTCTCCATATACGTGTCAAGACACCATTTCTCAATGG 336
DB 734 TTTTGTGTTTTTTCAGTACACAGCTCTCCATATACGTGTCAAGACACCATTTCTCAATGG 675

QY 337 AAGAAAGATTAGGAATAGTCCCAAGAGTTGCAATCTCTCAAGTCAGAAATATAAGC 396
DB 674 AAGAAAGATTAGGAATAGTCCCAAGAGTTGCAATCTCTCAAGTCAGAAATATAAGC 615

QY 397 TTGCAGGAAGTCTGCAGCATGTGGCTGAAAACTCTGTCGAGCTGTATACCAAGCTG 456
DB 614 TTGCAGGAAGTCTGCAGCATGTGGCTGAAAACTCTGTCGAGCTGTATACCAAGCTG 555

QY 457 GAGCACAGGTGCGAGCCCTGTACAGAAATGGAATGGATGGAGACAAATTCGTACC 516
DB 554 GAGCACAGGTGCGAGCCCTGTACAGAAATGGAATGGATGGAGACAAATTCGTACC 495

QY 517 AGTTCTATAGACAGCAAGAGTGGGAGGCTGTAAATATTTCTGCTTGTAGTGAAGT 576
DB 494 AGTTCTATAGACAGCAAGAGTGGGAGGCTGTAAATATTTCTGCTTGTAGTGAAGT 435

QY 577 CTACCATCTGAAGATAACAAACAGAAAGACCTGGAATTTGCGCGCTCTCAGAGCTACT 636
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QY 697 TGTGATGATGGAACCCCTTTTCACTCTGAACTGTTCCATATATATATAGATGTACCA 756
DB 314 TGTGATGATGGAACCCCTTTTCACTCTGAACTGTTCCATATATATATAGATGTACCA 255

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DB 254 GCCCAAGAACAGAGACTGTGTGGCCATCTCTTAATGGATGATCTTCTCAAGGAGTGA 195

QY 817 AAGAAATTCAGCGTTGTCTGTGAGAGAGGGCAGGAATGTTGAAGCCAGAGGCTCC 876

DB 194 AAGAAATTCAGCGTTGTCTGTGAGAGAGGGCAGGAATGTTGAAGCCAGAGGCTCC 135

QY 877 ATGTCCCCCTGAAACATTTAGCGCAAGTGACTGATTCGCCCTCTGCAACTACAAATAGC 936

DB 134 ATGTCCCCCTGAAACATTTAGCGCAAGTGACTGATTCGCCCTCTGCAACTACAAATAGC 75

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DB 74 AGAGTGAGCCAGCGGTGCCAAAGCAAGGGCTAGTT 39

RESULT 15
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LOCUS
DEFINITION BX324788 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI049YB09 5-PRIME, mRNA sequence.
ACCESSION BX324788
VERSION BX324788.2 GI:46271524
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 1001)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT On May 2, 2003 this sequence version replaced gi:30336406.
Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6541.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0AI049CA05QPI&c=6541.r.

FEATURES
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/clone="CS0DI049YB09"
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6
vector. Library was normalized."

ORIGIN

Query Match 48.1%; Score 855; DB 5; Length 1001;
Best Local Similarity 99.4%; Pred. No. 4.6e-226;
Matches 888; Conservative 1; Mismatches 1; Indels 3; Gaps 3;

QY 25 GGGCAATTCGACCATTTTCACTCTCACCGCTGTAGGAATCCAGATGAGCCAGTACA 84

DB 1 GGGCAATTCGACCATTTTCACTCTCACCGCTGTAGGAATCCAGATGAGCCAGTACA 60

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DB 61 GCAGCAGAGGACATGCTGGATGATGATGGGACACCAACCATGAGCTGCTTCTCAAG 120

QY 145 CCTCTGCCCAACTGCGGATCCAGAGCCCGCGCGCAGAGACACAGGCTCTCTTCAA 204

Db 121 GCTCTGCCACAACCTGGCATCCAGAGCCCGCGGCACAGACAGAGGCTCCCTCTCAA 180
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Search completed: October 8, 2005, 00:33:37
Job time : 5327 secs

Blank (uspio)

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 7, 2005, 20:59:17 : Search time 549.659 Seconds
(without alignments)
3015.556 Million cell updates/sec

Title: US-10-689-742-160

Perfect score: 1508

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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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3: Geneseqn2000s:*

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11: Geneseqn2003ds:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1508	100.0	1756	AAK94474	Human ful
2	1508	100.0	1756	ADL31263	Full leng
3	1508	100.0	1776	AAK33810	Coding se
4	1508	100.0	1841	AAK65072	Membrane-
5	1508	100.0	1841	AAK91561	Human PRO

ALIGNMENTS

RESULT 1

AAK94474

ID AAK94474 standard; cDNA; 1756 BP.

XX

AC AAK94474;

XX

DT 06-NOV-2001 (first entry)

XX

XX Human full-length cDNA, SEQ ID NO: 3296.

DB

XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX

OS Homo sapiens.

XX

PN EP1130094-A2.

XX

PD 05-SEP-2001.

XX

PF 07-JUL-2000; 2000EP-00114089.

XX

PR 08-JUL-1999; 99JP-00194486.

PR

PR 11-JAN-2000; 2000JP-00118774.

PR

PR 02-MAY-2000; 2000JP-00183765.

XX

PA (HELI-) HELIX RES INST.

XX

Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX

DR WPI; 2001-524255/58.
 XX P-PSDB; AAM93544.
 PT 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.

XX Claim 8; SEQ ID NO 3296; 1380pp + Sequence Listing; English.

XX The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesizing the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a full length human cDNA of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in CD-ROM format directly
 CC from EPO

SQ Sequence 1756 BP; 490 A; 427 C; 369 G; 470 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,09e-147 Length: 1756
 Score: 1508.00 Matches: 280
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-689-742-160 (1-280) x AAK94474 (1-1756)

Qy 1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspGlyAspThrMet 20
 Db 64 ATGCAGGCCCAAGTACAGCAGCAGCAGGACATGCTGGATGATGATGGGGACACCATG 123
 Qy 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40
 Db 124 AGCTGTCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCGGCGACAGAGCAC 183
 Qy 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuLeuVal 60
 Db 184 AGGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCTGCTGCTGCTGCTGCTG 243
 Qy 61 LeuLeuLeuGlyLeuAlaLeuAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsn 80
 Db 244 CTGCTGATAGGCTGGCGAGCCCTGGGGCTTTTGTGTTTTCAGTACTACCACTCTCCAAT 303
 Qy 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
 Db 304 ACTGGTCAAGACACCATTTCTCAATGAAGAAAGATAGGAATACGTCCCAAGAGTTG 363
 Qy 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120
 Db 364 CAATCTCTCAAGTCCAGATATAAAGCTTGCGAAGCTGCGACAGTGTGGCTGAAAAA 423
 Qy 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
 Db 424 CTCTGTCTGAGCTGTATAAACAGCTGGAGCACACAGGTGCGCCCTTGTACAGAACAA 483
 Qy 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
 Db 484 TGGAAATGGCATGGAGACAAATGTACAGTCTTATAAAGACAGCAAAAGTTGGAGGAC 543
 Qy 161 CysLysTyrPheCysLeuSerGlnAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
 Db 544 TGTAAATATTCTTGCTTAGTGAAACCTCTACCATGCTGAAGATAAACAAACAAAGAGAC 603
 Qy 181 LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu 200
 Db 604 CTGGAAATTTGGCGGCTCTCAGAGCTACTCTGAGTTTCTTCTACTCTTATTGACAGGGCTT 663

Qy 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
 Db 664 TTGGCCCTGACAGTGGCAAGGCTGGCTGTGGATGATGGAACCCCTTTCACTTCTGAA 723
 Qy 221 LeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu 240
 Db 724 CTGTTCCATATTATAATAGATGTCCACGAGCCCAAGAGCAGAGACTGTGTGGCCATCCTT 783
 Qy 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArg 260
 Db 784 AATGGATGATCTTCTCAAGGACTGCAAGAAATTGAAGCTTGTGTCTGTGAGAGAAG 843
 Qy 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280
 Db 844 GCAGGAATGGTGAAGCCAGAGAGCTCCTCATGTCCCCCTGAAACATTAGGCGAAGGTGAC 903

RESULT 2

ADL31263
 ID ADL31263 standard; cDNA; 1756 BP.

XX ADL31263;

XX AC ADL31263;

XX DT 20-MAY-2004 (first entry)

XX DE Full length human cDNA clone SeqID 3296.

XX KW human; medicine; signal transduction; glycoprotein; transcription;

XX KW oligo-capping method; ss; gene.

XX OS Homo sapiens.

XX XX EPI396543-A2.

XX XX 10-MAR-2004.

XX XX 07-JUL-2000; 2003EP-00025638.

XX PR 08-JUL-1999; 99JP-00194486.

XX PR 11-JAN-2000; 2000JP-00118774.

XX PR 02-MAY-2000; 2000JP-00183865.

XX PR 07-JUL-2000; 2000EP-00114089.

XX XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX XX Ota T. Nishikawa T. Isogai T. Hayashi K. Ishii S. Kawai Y.

XX XX Wakamatsu A. Sugiyama T. Nagai K. Kojima S. Otsuki T. Koga H.

XX XX WPI; 2004-204755/20.

XX XX P-PSDB; ADL31264.

XX XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full

XX XX length human cDNAs.

XX XX Example 1; SEQ ID NO 3296; 1340pp; English.

XX XX This invention relates to a novel primers useful for synthesizing full

XX XX length cDNA molecules that encode human proteins. Specifically, it refers

XX XX to secretory or membrane proteins that are potential therapeutic agents/

XX XX target molecules in the field of medicine, and in particular genes

XX XX encoding proteins that are associated with signal transduction,

XX XX glycoproteins and transcription. The present invention describes a method

XX XX for efficiently cloning a full length human cDNA from both the 5' and 3'

XX XX ends using the oligo-capping method. This polynucleotide sequence is a

SQ Sequence 1756 BP; 490 A; 427 C; 369 G; 470 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,09e-147 Length: 1756
 Score: 1508.00 Matches: 280
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0

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DB:          12          Gaps:          0
US-10-689-742-160 (1-280) x ADL31263 (1-1756)

QY 1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspGlyAspThrThrMet 20
DB 64 ATGCAGGCCAAGTACAGCAGCAGCAGGAGCATGCTGGATGATGGGGACACCAACCATG 123
QY 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40
DB 124 AGCCTGCAATCTCAAGCCTCTGCCCACTCGGCATCCAGAGCCCGCGGCACAGAGCAC 183
QY 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal 60
DB 184 AGGGCTCCCTCTTCAACGTGGGACAGCGGCCCTGACCCCTGACTTTGTGTGTGTG 243
QY 61 LeuLeuLeuGlyLeuAlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsn 80
DB 244 CTGCTGATAGGCTGGCAGCCCTGGGGCTTTTGTGTTTTCAGTACTACCAGCTCTCCAAT 303
QY 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
DB 304 ACTGGTCAAGACACCAATTTCTCAAAATGGAAGAAAGATTAGGAATACGTCCCAAGAGTTG 363
QY 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120
DB 364 CAATCTCTTCAAGTCAGAAATATAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAA 423
QY 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
DB 424 CTCTGTGTGAGCTGTATTAACAAAGCTGGAGCACACAGGTGCAGGCCCTGTACAGAACAA 483
QY 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
DB 484 TGGAAATGCGCATGGAGACAATTTGCTACCAAGTTCTATAAAGACAGCAAAAGTTGGAGGAC 543
QY 161 CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
DB 544 TGTAATATTTCTGCTTAGTGAAACTCTACCATGCTGAAGATAAACAAACAAAGAGAC 603
QY 181 LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu 200
DB 604 CTGGAAATTTGCGCGCTCTCAGAGCTACTCTGAGTTTCTACTCTTATTGGACAGGGTT 663
QY 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
DB 664 TTGCGCCCTTGACAGTGGCAAGCCCTGGCTGTGGATGGATGGAACCCCTTTCACCTCTCAA 723
QY 221 LeuPheHisIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu 240
DB 724 CTGTTTCCATATTATTAATAGATGTCACCAAGCCCAAGACAGAGACTGTGTGGCCATCTTT 783
QY 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
DB 784 AATGGATGATCTTCTCAAGACTGCAAGAAATTTGAAGCGTTGTCTGTGAGAGAGG 843
QY 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280
DB 844 GCAGGAATGGTGAAGCCAGAGAGCTCCATGTGTCCTCCCTGAAACATTAGGCGAAGGTGAC 903

RESULT 3
AA333810
ID AAX33810 standard; DNA; 1776 BP.
XX
AC AAX33810;
XX
XX
DT 25-JUN-1999 (first entry)
XX
DE Coding sequence for human secreted protein bn97_1.
XX
DE Secreted protein; human; nutritional activity; cytokine; tissue growth;
KW cell proliferation; cell differentiation; immune stimulant; chemotaxis;
KW immune suppressant; haematopoiesis regulator; activin; inhibin; cadherin;

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KW chemokinesis; haemostasis; thrombolysis; anti-inflammatory; gene therapy;
XX tumour invasion suppressor; tumour inhibitor; ss.
OS Homo sapiens.
XX WO9913066-A1.
XX 18-MAR-1999.
XX 08-SEP-1998; 98WO-US018724.
XX 08-SEP-1997; 97US-00929007.
XX (GENY ) GENETICS INST INC.
XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Evans C, Merberg D;
PI Treacy M, Agostino MJ, Spaulding V;
XX WPI; 1999-229235/19.
DR P-PsDB; AAY03317.
XX
XX New polynucleotides encoding secreted human proteins.
PS Claim 1; Page 78; 96pp; English.
XX
XX This sequence encodes a human secreted protein of the invention. The
CC secreted proteins were obtained from human adult placenta, foetal brain,
CC adult testes or adult blood cDNA libraries. The polynucleotides (PNs) and
CC proteins are predicted to have biological activities which would make
CC them suitable for treating, preventing or ameliorating medical conditions
CC in humans and animals, although no supporting data is given. Suggested
CC activities include nutritional activity, cytokine and cell
CC proliferation/differentiation activity, immune stimulating (e.g. as
CC vaccines) or suppressing activity, haematopoiesis regulating activity,
CC tissue growth activity, activin/inhibin activity,
CC chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,
CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumour
CC invasion suppressor activity, and tumour inhibition activity. The PNs are
CC also stated to be useful for gene therapy
XX
SQ Sequence 1776 BP; 506 A; 429 C; 370 G; 471 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.14e-147 Length: 1776
Score: 1508.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-689-742-160 (1-280) x AAX33810 (1-1776)
QY 1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspGlyAspThrThrMet 20
DB 69 ATGCAGGCCAAGTACAGCAGCAGCAGGAGCATGCTGGATGATGGGGACACCAACCATG 128
QY 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40
DB 129 AGCCTGCAATCTCAAGCCTCTGCCCACTCGGCATCCAGAGCCCGCGGCACAGAGCAC 188
QY 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal 60
DB 189 AGGGCTCCCTCTTCAACGTGGGACAGCGGCCCTGACCCCTGCTGACTTTGTGTGTGTG 248
QY 61 LeuLeuLeuGlyLeuAlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsn 80
DB 249 CTGCTGATAGGCTGGGACGCCCTGGGGCTTTTGTGTTTTCAGTACTACCAGCTCTCCAAT 308
QY 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
DB 309 ACTGGTCAAGACACCAATTTCTCAAAATGGAAGAAAGATTAGGAATACGTCCCAAGAGTTG 368
QY 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120

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Db      369  CAATCTCTCAAGTCAGAAATAAAGCTTGCCAGCAAGTCTGCAGCATGTGGCTGAAAAA 428
QY      121  LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
Db      429  CTCGTGCTGAGCTGTATAACAAAGCTGGAGCACACAGGTGAGCCCTTGACAGAACAA 488
QY      141  TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
Db      489  TGGAAATGGCATGGAGACAATTGCTACCAAGTCTATATAAGACAGCAAAAGTTGGAGGAC 548
QY      161  CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
Db      549  TGTAAATATTTCTGCTTAGTGAAAACTCTACCATGCTGAAGATAAAACAAACAAGAGAC 608
QY      181  LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu 200
Db      609  CTGGAATTTGGCGGTCTCAGAGCTACTCTGAGTTTTCTACTCTTTATGGACAGGGCTT 668
QY      201  LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
Db      669  TTGGCCCTGACAGTGGCAAGSCCTGGCTGTGGATGGATGGACCCCTTTCACTTCGAA 728
QY      221  LeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu 240
Db      729  CTGTTCCATATTATAATAGATGTCACCAAGCCCAAGACAGACAGACTGTGTGGCCATCCTT 788
QY      241  AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
Db      789  AATGGATGATCTTCTCAAGACTGCAAGAAATGAAGCGTTGTGTCTGTGAGAGAGG 848
QY      261  AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280
Db      849  GCAGGAATGGTGAAGCCAGAGAGCTCCATGTCCCCCTGAAACATAGGCGAAGGTGAC 908

RESULT 4
AAZ65072
ID      AAZ65072 standard; cDNA; 1841 BP.
XX
AC      AAZ65072;
XX
DT      05-APR-2000 (first entry)
XX
DE      Membrane-bound protein PRO1131 encoding cDNA.
XX
KW      Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW      pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX
OS      Homo sapiens.
XX
PN      WO9963088-A2.
XX
PD      09-DEC-1999.
XX
PF      02-JUN-1999; 99WO-US012252.
XX
PR      02-JUN-1998; 98US-0087607P.
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PR      02-JUN-1998; 98US-0087759P.
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PR      04-JUN-1998; 98US-0088025P.
PR      04-JUN-1998; 98US-0088028P.
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PR      05-JUN-1998; 98US-0088217P.
PR      09-JUN-1998; 98US-0088655P.
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PR      09-JUL-1998; 98US-0092182P.
PR      10-JUL-1998; 98US-0092472P.
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PR 20-JUL-1998; 98US-0093333P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
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PR 04-AUG-1998; 98US-0095301P.
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PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
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PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
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PR 17-AUG-1998; 98US-0096895P.
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PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.
XX (GETH ) GENENTECH INC.
XX
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX WPI; 2000-072883/06.
XX P-PSDB; AAY66728.
XX
PT Membrane-bound proteins and related nucleotide sequences.
XX
XX Claim 2; Fig 229; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
XX identified based on extracellular domain homology screening. The PRO
XX sequences have homology with proteins including LDL receptors, TIE
XX ligands and various enzymes. The membrane-bound proteins and receptor
XX molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX immunoadhesins, for instance, can be used as therapeutic agents to block
XX receptor-ligand interactions. The membrane-bound proteins can also be
XX employed for screening of potential peptide or small molecule inhibitors
XX of the relevant receptor/ligand interaction. The PRO encoding sequences
XX are useful as hybridization probes, in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA. PRO nucleic acid sequences will
XX also be useful for the preparation of PRO polypeptides, especially by
XX recombinant techniques
```

```
XX SQ Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3.3e-147 Length: 1841
Score: 1508.00 Matches: 280
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-689-742-160 (1-280) x AAZ65072 (1-1841)
QY 1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspGlyAspThrThrMet 20
DB 144 ATGCAGGCCAAGTACAGCAGCAGCAGGACATGCTGGATGATGATGGGACACACCATG 203
QY 21 SerLeuHisSerGlnAlaSerAlaThrArgHisProGluProArgArgThrLuhis 40
DB 204 AGCCTGCATTCTCAAGCCTCTGCCCACTCCAGAGCCCGCGCCAGAGGAC 263
QY 41 ArgAlaProSerSerThrTrrArgProValAlaLeuThrLeuThrLeuCysLeuVal 60
DB 264 AGGCTCCCTCTTCAAGTGGGACCACTGGCCCTGACCTGCTGCTTGTGCTGTG 323
QY 61 LeuLeuLeuGlyLeuAlaAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsn 80
DB 324 CTGCTGATAGGCTGGCAGCCCTGGGGCTTTGTTTTTTCAGTACTACCAAT 383
QY 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnLeu 100
DB 384 ACTGGTCAAGACACCACTTTCTCAATGGAGAAAGATTAGGAATACGTCCTCAAG 443
QY 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120
DB 444 CAATCTCTTCAAGTCCAGATATATAAGCTTCAGAGAAAGTCTGCAGCATGTGGCTG 503
QY 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
DB 504 CTCTGTGCTGAGCTGTATACAAAGCTGGAGCACACAGGTGACGCCCTTGTACAGAAC 563
QY 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
DB 564 TGGAAATGGCATGGAGCAATTTGTACCAAGTTCTATAAAGACAGCAAAAGTTGGAG 623
QY 161 CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
DB 624 TGTAAATATTTCTGCTTAGTGAATACTTACCAATGCTGAAGATAAACAACAAGAG 683
QY 181 LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu 200
DB 684 CTGGAAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAG 743
QY 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
DB 744 TTGCGCCCTGACAGTGGCAAGGCCCTGGCTGTGGATGGATGGAAACCCCTTTTCA 803
QY 221 LeuPheHisIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu 240
DB 804 CTGTTCCATATTATATAGATGTCCACCGCCCAAGAGCAGAGACTGTGTGGCCAT 863
QY 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArg 260
DB 864 AATGGGATGATCTTCTCAAGGACTGCAAGAAATTGAAGCGTTGTGTCTGTGAGAG 923
QY 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluAsp 280
DB 924 GCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCTCGAAACATTAGGCGA 983
XX RESULT 5
XX AAC91561
XX ID AAC91561 standard; cDNA; 1841 BP.
XX
```


KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
 KW A-peptide; factor VIIa; gene therapy; ss.

XX Homo sapiens.

XX WO200140466-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000WO-US032678.

XX 01-DEC-1999; 99WO-US028301.

XX 01-DEC-1999; 99WO-US028634.

XX 02-DEC-1999; 99WO-US028551.

XX 02-DEC-1999; 99WO-US028564.

XX 02-DEC-1999; 99WO-US028565.

XX 09-DEC-1999; 99US-0170262P.

XX 16-DEC-1999; 99WO-US030095.

XX 20-DEC-1999; 99WO-US030911.

XX 20-DEC-1999; 99WO-US030999.

XX 30-DEC-1999; 99WO-US031243.

XX 30-DEC-1999; 99WO-US031274.

XX 05-JAN-2000; 2000WO-US000219.

XX 06-JAN-2000; 2000WO-US000277.

XX 06-JAN-2000; 2000WO-US000376.

XX 11-FEB-2000; 2000WO-US003565.

XX 18-FEB-2000; 2000WO-US004341.

XX 18-FEB-2000; 2000WO-US004342.

XX 22-FEB-2000; 2000WO-US004414.

XX 24-FEB-2000; 2000WO-US004914.

XX 24-FEB-2000; 2000WO-US005004.

XX 01-MAR-2000; 2000WO-US005601.

XX 02-MAR-2000; 2000WO-US005841.

XX 03-MAR-2000; 2000US-0187202P.

XX 10-MAR-2000; 2000WO-US006319.

XX 15-MAR-2000; 2000WO-US006884.

XX 21-MAR-2000; 2000WO-US007377.

XX 21-MAR-2000; 2000WO-US007532.

XX 30-MAR-2000; 2000WO-US008439.

XX 17-MAY-2000; 2000WO-US013705.

XX 22-MAY-2000; 2000WO-US014042.

XX 30-MAY-2000; 2000WO-US014941.

XX 02-JUN-2000; 2000WO-US015264.

XX 05-JUN-2000; 2000US-0209832P.

XX 28-JUL-2000; 2000WO-US020710.

XX 11-AUG-2000; 2000WO-US022031.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 08-NOV-2000; 2000WO-US030952.

XX 10-NOV-2000; 2000WO-US030873.

XX (GETH) GENENTECH INC.

XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff B, Gao W;

XX Gerritsen ME, Goddard A, Godowski PU, Gurney AL, Sherwood S;

XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2001-408281/43.

XX P-PSDB; AAU12400.

XX Isolated , secretory and transmembrane PRO polypeptide used to detect
 other PRO polypeptides, link bioactive molecules to cells expressing PRO
 polypeptides, and detect the presence of mammalian tumors e.g. lung,
 breast, prostate, cervical.

XX Claim 3; Fig 457; 813pp; English.

XX AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
 polypeptides. The PRO polypeptides are useful to detect other PRO

XX polypeptides, to link bioactive molecules to cells expressing PRO

XX polypeptides, to modulate biological activities of cells expressing PRO

XX polypeptides, and to detect the presence of mammalian lung, colon,

CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 XX

SQ Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.3e-147 Length: 1841
 Score: 1508.00 Matches: 280
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-689-742-160 (1-280) x AAS21472 (1-1841)

QY 1 MetGlnAlaValTyrSerThrArgAspMetLeuAspAspGlyAspThrMet 20

DB 144 ATGCAGGCCAAGTACAGCAGCAGGAGACATCTGGATGATGGGACACCCATG 203

QY 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgThrGluHis 40

DB 204 AGCCTGCATTCTCAAGCCTCTGCCACAACCTGGCATCCAGACCCCGCCACAGAGCAC 263

QY 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal 60

DB 264 AGGGCTCCCTCTTCAACCTGGCAGCCAGTGGCCCTGACCTGCTGACTTTGTGTGGTG 323

QY 61 LeuLeuIleGlyLeuAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsn 80

DB 324 CTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTCTTCTAGTACTACAGCTCTCCAT 383

QY 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100

DB 384 ACTGCTCAAGACACCCATTCTCAATGGAAGAAATAGGAAATACGTCCCAAGAGTTG 443

QY 101 GlnSerLeuGlnValGlnAsnIleLeuLeuAlaGlySerLeuGlnHisValAlaGluLys 120

DB 444 CAATCTCTTCAAGTCCAGATATATAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAA 503

QY 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140

DB 504 CTCTGCTGAGCTGTATTAACAAGCTGGAGCACACAGTGGAGCCCTTGTACAGAACA 563

QY 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160

DB 564 TGGAAATGGCATGGAGACAATTTGCTACCAATTCATATAAGACAGCAAAAGTTGGGAGGAC 623

QY 161 CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180

DB 624 TGTAAATATTTCTGCTTTAGTGAAGAACTCTACCATGCTGAAGATAAACAAACAAGAGAC 683

QY 181 LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu 200

DB 684 CTGGAATTTGCCGCTCTCAGAGCTACTCTGAGTTTCTTACTCTTATTGGACAGGGCTT 743

QY 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220

DB 744 TTGGCCCTGACAGTGGAAGCCCTGGCTGTGGATGGATGGAAACCCCTTTTCACTTCTGAA 803

QY 221 LeuPheHisIleIleLeuAspValThrSerProArgSerArgAspCysValAlaIleLeu 240

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Db 804 CTGTTCCATATTATATAGATGTCCACGAGCCCAAGACGAGACTGTGTGCGCCATCCTC 863
Qy 241 AenGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArg 260
Db 864 AATGGATGAUCTTCTCAAGAGCTGCAAGATTTGAAGCGTTGTCTGTGAGAGAAGG 923
Qy 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280
Db 924 GCAGGAATGGTGAAGCCAGAGAGCTCCATGTCTCCCTGAAACATTAGGCGNAGGTGAC 983

RESULT 7
AAS46225
ID AAS46225 standard; cDNA; 1841 BP.
XX
XX AAS46225;
XX
XX 18-DEC-2001 (first entry)
XX
DE Human DNA encoding PRO polypeptide sequence #301.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194449P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
```

```
PR 20-DEC-2000; 2000WO-US034956.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-602746/68.
XX P-PSDB; AAU29324.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
XX presence of tumors, such as prostate and breast tumors, in mammals and to
XX screen for modulators of the compounds.
XX
XX Claim 2; Fig 601; 774pp; English.
XX
XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
XX primers for PRO polypeptides of the invention. The sequences of the
XX invention can be used to detect the presence of a tumour in a mammal by
XX comparing the level of expression of a PRO polypeptide in a test sample
XX of cells from the animal and a control sample of normal cells, whereby a
XX higher level of expression in the test sample indicates the presence of a
XX tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
XX pigs, goats and rabbits but are preferably human. The polypeptides can be
XX used to stimulate tumour necrosis factor (TNF) alpha release from human
XX blood, when contacted with it. A specific polypeptide can be used to
XX stimulate the proliferation or differentiation of chondrocyte cells. The
XX PRO proteins can be used to determine the presence of tumours and also
XX susceptibility to tumour development, particularly adrenal, lung, colon,
XX breast, prostate, rectal, cervical, or liver tumours, in mammalian
XX subjects. The oligonucleotide probes specific for the PRO nucleic acids
XX can be used for genetic analysis of individuals with genetic disorders
XX
XX SQ Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;
```

Alignment Scores:

```
Pred. NO.: 3.3e-147 Length: 1841
Score: 1508.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-689-742-160 (1-280) x AAS46225 (1-1841)

Qy 1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspGlyAspThrThrMet 20
Db 144 ATGCAGGCCAAAGTACAGCAGCAGGAGACATGCTGGATGATGATGGGACACACCAATG 203
Qy 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40
Db 204 AGCCTGCATTCTCAAGCCTCTGCCCAACTCGGCATCCAGAGCCCGCGCACAGAGCAC 263
Qy 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal 60
Db 264 AGGGCTCCCTCTTCAACGTCGCGACCAAGTGGCCCTGACCCCTGCTGACTTTTGTGTGTG 323
Qy 61 LeuLeuIleGlyLeuAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsn 80
Db 324 CTGCTGATAGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACCACTCTCCANT 383
Qy 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
Db 384 ACTGTCAGACACCACTTTCTCAATGGAGAAAGATTAGGAATACGTGCCAAGAGTTG 443
Qy 101 GlnSerLeuGlnValGlnAlaSerIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120
Db 444 CAATCTCTTCAAGTCCAGAAATATAAGCTTCAGAGAGTCTGCAGCATGTGGCTGAAAAA 503
Qy 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
Db 504 CTCTGTCTGAGCTGTATACAAAGAGCTGGAGCACACAGGTGACGCCCTTGTACAGAACAA 563
```

QY 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
 Db 564 TCGAAATGGCATGGAGACAAATGCTACCACTTCTATAAAGACAGCAAAAGTTGGAGGAC 623
 QY 161 CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysLeuAsnLysGlnGluAsp 180
 Db 624 TGTAAATATTTCTGCTTAGTGAATACTCTACATGCTGAAGATTAACAAACAGAGAC 683
 QY 181 LeuGluPheAlaAsnSerGlnSerTyrSerGluPhePheTyrSerTrpTrpThrGlyLeu 200
 Db 684 CTGGAATTTGGCGCTCTCAGAGCTACTCTGAGTTTCTACTCTTATTGGACAGGCTT 743
 QY 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
 Db 744 TTGCGCCCTTCAGAGTGGCAAGCCCTGGCTGTGATGGATGGAACCCCTTCTCTGAA 803
 QY 221 LeuPheHisIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu 240
 Db 804 CTGTTCCATATTAATAGATGTACAGCCCAAGACAGAGACTGTGTGGCCATCTCTC 863
 QY 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArg 260
 Db 864 AATGGATGATCTTCTCAAGGACTGCAAGAAATGAAGCGTTGTCTGTGAGAGAAG 923
 QY 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluAsp 280
 Db 924 GCAGGAATGGTGAAGCAGAGAGCCTCCATGTCTCCCTGAAACATTAGGCGAAGGTGAC 983
 RESULT 8
 AAF44218
 ID AAF44218 standard; cDNA; 1841 BP.
 XX AC AAF44218;
 XX DT 02-APR-2001 (first entry)
 XX DE Human PRO1131 (UNQ569) nucleotide sequence SEQ ID NO:318.
 KW Human; secreted and transmembrane protein; PRO; cytotstatic; cell death;
 KW cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay; ss.
 XX OS Homo sapiens.
 XX PN WO200073454-A1.
 XX PD 07-DEC-2000.
 XX PF 30-MAR-2000; 2000WO-US008439.
 XX PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 07-JUL-1999; 99US-0143048P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 08-OCT-1999; 99US-0158663P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.

PR 20-MAR-2000; 2000WO-US007377.
 XX (GETH) GENENTECH INC.
 XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoletti NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams FM, Wood WI;
 PI Zhang Z;
 XX WPI; 2001-032160/04.
 DR P-PSDB; AAB65251.
 XX PT PRO polynucleotides used to produce polypeptides used to target bioactive
 PT molecules such as toxins, radiolabels or antibodies, to specific cells,
 PT to cause targeted cell death.
 XX Claim 2; Fig 229; 935pp; English.
 XX CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytotstatic activity. The PRO proteins can
 CC be used for targeted delivery of bioactive molecules, such as toxins,
 CC radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
 CC DNA. They may also be used to produce transgenic animals which are used
 CC to develop and screen therapeutically useful reagents. The PRO nucleotide
 CC and protein sequence can be used for tissue typing and in treating
 CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
 CC AAF44470 represent PCR primers and hybridisation probes used in the
 CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
 CC AAB65300 represent human PRO polynucleotide and protein sequences given
 CC in the exemplification of the present invention
 XX SQ Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3.3e-147 Length: 1841
 Score: 1508.00 Matches: 280
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0
 US-10-689-742-160 (1-280) x AAF44218 (1-1841)
 QY 1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspGlyAspThrMet 20
 Db 144 ATGCAGGCCAAGTACAGCAGCAGCAGGACATGCTGGATGATGGGACACCCATG 203
 QY 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40
 Db 204 AGCTGTCATTTCTCAAGCTCTGCCCACTCGGCATCCAGAGCCCGGGCAGAGCAGC 263
 QY 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuVal 60
 Db 264 AGGGCTCCCTCTTCAACGTCGACAGTGGCCCTGACCTGCTGCTGCTGCTGCTG 323
 QY 61 LeuLeuIleGlyLeuAlaAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsn 80
 Db 324 CTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTGTTTTTTCAGTACTACCACTCTCCAAT 383
 QY 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
 Db 384 ACTGTCAGACACCACTTTCTCAATGGAGAGAGATAGGAATACGTCCTCCAGAGTTG 443
 QY 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValaGluLys 120
 Db 444 CAATCTCTCAAGTCCAGATATAAAGCTTGCAGGAAGTCTGCAGAGTGTGGCTGA 503
 QY 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
 Db 504 CTCTGCTGAGCTGTATACAAAGCTGGAGCACAGGTGAGCCCTTTGTACAGAACAA 563

QY 141 TplYsTTPHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTyrGluuAsp 160
 DB 564 TGGAAATGGCATGGAGACAAATGCTACCAAGTCTATAAAGACAGCAAAAGTTGGAGGAC 623
 QY 161 CysLysTyrPheCysLeuSerGluuAsnSerThrMetLeuLysIleAsnLysGlnGluuAsp 180
 DB 624 TGTAAATATTCTGCCTTAGTCTGAAACTCTACCATGCTGAAGATAAACAACAAGAGAC 683
 QY 191 LeuGluPheAlaAlaSerGlnSerTyrSerGluuPhePheTyrSerTyrTyrThrGlyLeu 200
 DB 684 CTGGAATTTGGCGCGCTCTCAGAGCTACTCTGAGTTTCTTACTCTTATTTGACAGGGCTT 743
 QY 201 LeuArgProAspSerGlyLysAlaTyrLeuTyrMetAspGlyThrProPheThrSerGlu 220
 DB 744 TTGGCCCTGACAGTGGCAAGCCCTGGCTGGATGGATGGAACCCCTTCTACTCTGAA 803
 QY 221 LeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu 240
 DB 804 CTGTTCCATATTATAATAGATGTCAACAGCCCAAGACAGAGACTGTGTGCCATCTC 863
 QY 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluuArg 260
 DB 864 AATGGATGATCTTCTCAAGAGACTGCAAGAAATGGAAGCGTTGTCTGTGAGAGAGG 923
 QY 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280
 DB 924 GCAGGAATGGTGAAGCCAGAGAGCTCCATGTCCCCCTGAAACATTAGGCGAAGTGAC 983
 RESULT 9
 ID ABL88154 standard; cDNA; 1841 BP.
 XX ABL88154;
 AC ABL88154;
 XX 16-MAY-2002 (first entry)
 XX Human PRO1131 cDNA sequence SEQ ID NO:165.
 XX Human; angiogenesis; cardiast; cytostatic; antiangiogenic; hypotensive;
 KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping; gene; ss.
 XX Homo sapiens.
 OS
 XX
 XX WO200200690-A2.
 PN
 XX
 XX 03-JAN-2002.
 PD
 XX
 XX 20-JUN-2001; 2001WO-US019692.
 XX
 XX 23-JUN-2000; 2000US-0213637P.
 PR 23-JUN-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 18-SEP-2000; 2000US-0064357.
 PR 17-AUG-2000; 2000US-0064357.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-0070923P.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Paoni NP;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Watanabe CK, Williams PM, Wood WI, Ye W;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI; 2002-090516/12.
 DR P-PSDB; ABB84899.
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX Claim 2; Fig 165; 565pp; English.
 PS
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3.3e-147 Length: 1841
 Score: 1508.00 Matches: 280
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-689-742-160 (1-280) x ABL88154 (1-1841)

QY 1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspGlyAspThrThrMet 20
 DB 144 ATGCAGGCCAAGTACAGCAGCGAGGACATGCTGGATGATGATGGGACACCATG 203
 QY 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40
 DB 204 AGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCGCGCAGACGAC 263
 QY 41 ArgAlaProSerSerThrThrArgProValAlaLeuThrLeuLeuCysLeuVal 60
 DB 264 AGGCGTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCTGCTGACTTTGTGCTGGTG 323

QY 61 LeuLeuIleGlyLeuAlaLeuGlyLeuPhePheGlnTyrTyrGlnLeuSerAen 80
 Db 324 CTGCTCATAGGGCTGGCAGCCCTGGGGCTTTGTTTTTTCAGTACTACAGCTCTCCAAT 383
 QY 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyValAsnThrSerGlnGluLeu 100
 Db 384 ACTGGTCAAGACACCACTTTCTCAATGGGAAGAAGATTAGGAATAACGTCCTCCAGAGTTG 443
 QY 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120
 Db 444 CAATCTCTTCAAGTCCAGAAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAA 503
 QY 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
 Db 504 CTCTGTCGTGAGCTGTATACAAAGCTGGAGCACAAGGTGCAGCCCTTGTACAGAACAA 563
 QY 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
 Db 564 TGGAAATGGCATGGAGACAAATGCTACCAAGTCTATTAAGACAGCAAAAGTTGGAGGAC 623
 QY 161 CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
 Db 624 TGTAAATATTCTGCTTGTAGTGAAGAACTTACCATGCTGAAGATAAACAAACAAGAGAC 683
 QY 181 LeuGluPheAlaLeuSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu 200
 Db 684 CTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTT 743
 QY 201 LeuArgProAspSerGlyLysAlaTrpLeuTyrMetAspGlyThrProPheThrSerGlu 220
 Db 744 TTGGCCCTTGACAGTGGCAAGCGCTGGCTGTGATGGATGGAAACCCCTTTCATCTGAA 803
 QY 221 LeuPheHisIleIleLeuAspValThrSerProArgSerArgAspCysValAlaLeu 240
 Db 804 CTGTTCCATATTATAATAGATGTACACAGCCCAAGAAAGCAGAGACTGTGTGGCCATCTC 863
 QY 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
 Db 864 AATGGATGATCTTCTCAAGGACTGCAAGAAGATTGAACGTTGTGTGTGAGAGAAGG 923
 QY 261 AlaGlyMetValLysProGluSerLeuHisValProGluThrLeuGlyGluAsp 280
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 ID ABL95643 standard; cDNA; 1841 BP.
 AC ABL95643;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE Human angiogenesis related cDNA PRO1131 SEQ ID NO: 165.
 XX
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiac; cytostatic; antiangiogenic; hypotensive; vulnery;
 KW antiarteriosclerotic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200208284-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 09-JUL-2001; 2001WO-US021735.
 XX
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-00643657.

PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006665.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
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 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 XX (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M B.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI; 2002-171999/22.
 DR P-PSDB; ABB95505.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 PS Claim 1; Fig 165; 567pp; English.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a coding sequence of the invention
 XX
 SQ Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;
 Alignment Scores: 3..3e-147 Length: 1841
 Pred. No.:

Score: 1508.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-689-742-160 (1-280) x ABL95643 (1-1841)

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DB 144 ATGACAGCCAGTACAGCAGCAGCAGCAGCAGTCTGGATGATGGGACACACCATG 203
QY 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40
DB 204 AGCTTGCATTTCTCAAGCCTCTGCCAATCGGCATCCAGAGCCCGCGCACAGACAC 263
QY 41 ArgAlaProSerSerThrTyrArgProValAlaLeuThrLeuThrLeuThrLeuVal 60
DB 264 AGGGCTCCCTCTTCAACGTGGCGACGATGGCCCTGCACCTGTGCTGTGTGTG 323
QY 61 LeuLeuIleGlyLeuAlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsn 80
DB 324 CTGCTGATAGGCTGGCAGCCCTGGGCTTTTGTCTTTTTCAGTACTACAGCTCTCCAT 383
QY 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
DB 384 ACTGGTCAAGACACCATTTCTCAATGGAAGAAAGATTAGGAAATACGTCCTCAAGATTG 443
QY 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120
DB 444 CAATCTCTTCAAGTCCAGAAATATAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAA 503
QY 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
DB 504 CTCTGCTGCTGCTGTATTAACAGCTGGAGCACACAGTGCAGCCCTGTGTACAGAACAA 563
QY 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
DB 564 TGGAAATGGCATGGAGACAATTCGTACCAAGTTCTATAAAGACAGCAAAAGTTGGAGGAC 623
QY 161 CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnLysAsp 180
DB 624 TGTAATAATTTCTGCTTGTAGTAAACCTTACCATGCTGAAGATATAACAAAGAACAGAC 683
QY 181 LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTyrThrGlyLeu 200
DB 684 CTGGAAATTTGGCGCTCTCAGAGCTACTCTGAGTTTCTACTCTTATGGACAGGGCTT 743
QY 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
DB 744 TTGGCCCTGCAGTGGCAAGCCCTGGCTGGATGGATGGAACCCCTTTCATCTCTGAA 803
QY 221 LeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu 240
DB 804 CTGTTCCATATATATATAGATGTCCAGGCCCAAGACAGAGACTGTGTGGCCATCTCTC 863
QY 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
DB 864 AATGGATGATCTTCTCAAGACTGCAAGAAATGAAGCGTTGTCTGTGAGAGAGG 923
QY 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280
DB 924 GCAGGAATGGTGAAGCCAGAGAGCCTCCATGTGCCCCCTGAAACATTAGGCGAAGGTGAC 983
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RESULT 11

ACA89675

ID ACA89675 standard; cDNA; 1841 BP.

XX AC
XX ACA89675;

DT 10-JUL-2003 (first entry)

DE cDNA encoding human PRO polypeptide #301.

XX Human; PRO polypeptide; secreted protein; transmembrane protein;
KW Chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast;
KW prostate; rectal; cervical; liver; cancer; TNF-alpha;
KW tumour necrosis factor-alpha; proliferation; differentiation;
KW chondrocyte cell; bone disorder; cartilage disorder; sports injury;
KW arthritis; cytostatic; antiarthritic; osteopathic; gene therapy; gene;
ss.
XX Homo sapiens.
XX OS
XX US2003036141-Al.
XX PD
XX 20-FEB-2003.
XX PF
XX 01-JUL-2002; 2002US-00187597.
XX 18-SEP-1997; 97US-0059263P.
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PR 01-APR-1998; 98US-0080327P.
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PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
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PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.

XX Human; PRO polypeptide; secreted protein; transmembrane protein;
KW Chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast;
KW prostate; rectal; cervical; liver; cancer; TNF-alpha;
KW tumour necrosis factor-alpha; proliferation; differentiation;
KW chondrocyte cell; bone disorder; cartilage disorder; sports injury;
KW arthritis; cytostatic; antiarthritic; osteopathic; gene therapy; gene;
ss.
XX Homo sapiens.
XX OS
XX US2003036141-Al.
XX PD
XX 20-FEB-2003.
XX PF
XX 01-JUL-2002; 2002US-00187597.
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PR 01-APR-1998; 98US-0080327P.
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PR 22-APR-1998; 98US-0082797P.
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PR 29-APR-1998; 98US-0083496P.
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PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
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PR 15-MAY-1998; 98US-0085579P.
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PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.


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QY      101  GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120
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Db      444  CAATCTCTTCAAGTCAGAAATATAAAGCTTGACGAGAGTCTGCAGCATGTGGCTGAAAAA 503

QY      121  LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
      |||||
Db      504  CTCCTGCTGAGCTGTATTAACAAAGCTGGAGCACACAGGTGCGCCCTTGACAGAACAA 563

QY      141  TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
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Db      564  TGGAAATGGCATGGAGACAAATGCTACCACTTCTATTAAGACAGCAAAAGTTGGAGGAC 623

QY      161  CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
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Db      624  TGTAAATATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAAAACAACAAGAGAC 683

QY      191  LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu 200
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Db      684  CTGGAATTTGGCGGCTCTCAGAGCTACTCTGAGTTTCTTACTCTTATTGGACAGGGCTT 743

QY      201  LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
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QY      221  LeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu 240
      |||||
Db      804  CTGTTCCATATTATAATAGATGTCAACAGCCCAAGACAGAGACTGTGTGGCCATCCTC 863

QY      241  AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
      |||||
Db      864  AATGGGATGATCTTCTCAAGAGACTGCAAGAAATTGAAGCGTTGTCTGTGAGAGAAAG 923

QY      261  AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280
      |||||
Db      924  GCAGGAATGGTGAAGCCAGAGAGCCCTCATGTGCCCCCTGAAACATTAGGCGAAGTGAC 983

RESULT 12
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ID ACA73685 standard; cDNA; 1841 BP.
XX
AC ACA73685;
XX
XX
DT 01-JUL-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) cDNA #301.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW proliferation; differentiation; chondrocyte cells;
KW tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
XX
OS Homo sapiens.
XX
XX US2003036146-A1.
XX
PD 20-FEB-2003.
XX
XX
PF 02-JUL-2002; 2002US-00187603.
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PR 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-000311832.
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PR      14-MAY-1999; 99WO-US010733.
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PR      25-AUG-1999; 99US-00380137.
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PR      01-SEP-1999; 99WO-US020111.
PR      15-SEP-1999; 99WO-US021090.
PR      18-OCT-1999; 99US-00403297.
PR      12-NOV-1999; 99US-00423844.
PR      01-DEC-1999; 99WO-US028301.
PR      02-DEC-1999; 99WO-US028551.
PR      30-DEC-1999; 99WO-US031274.
PR      05-JAN-2000; 2000WO-US000219.
PR      18-FEB-2000; 2000WO-US004341.
PR      18-FEB-2000; 2000WO-US004342.
PR      22-FEB-2000; 2000WO-US004414.
PR      24-FEB-2000; 2000WO-US005004.
PR      01-MAR-2000; 2000WO-US005601.
PR      02-MAR-2000; 2000WO-US005841.
PR      15-MAR-2000; 2000WO-US006884.
PR      30-MAR-2000; 2000WO-US008439.
PR      17-MAY-2000; 2000WO-US013705.
PR      22-MAY-2000; 2000WO-US014042.
PR      30-MAY-2000; 2000WO-US014941.
PR      02-JUN-2000; 2000WO-US015264.
PR      28-JUL-2000; 2000WO-US020710.
PR      22-AUG-2000; 2000US-00844848.
PR      24-AUG-2000; 2000WO-US023328.
PR      18-SEP-2000; 2000US-00664610.
PR      18-SEP-2000; 2000US-00665350.
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PR      01-DEC-2000; 2000WO-US032678.
PR      20-DEC-2000; 2000US-00747259.
PR      20-DEC-2000; 2000WO-US034956.
PR      28-FEB-2001; 2001WO-US006520.
PR      22-MAR-2001; 2001US-00816744.
PR      10-MAY-2001; 2001US-00854208.
PR      10-MAY-2001; 2001US-00854280.
PR      25-MAY-2001; 2001US-00866028.
PR      01-JUN-2001; 2001WO-US017800.
PR      05-JUN-2001; 2001US-00874503.
PR      20-JUN-2001; 2001WO-US019692.
PR      29-JUN-2001; 2001WO-US021066.
PR      09-JUL-2001; 2001WO-US021735.
PR      18-JUL-2001; 2001US-00908827.
PR      30-JUL-2001; 2001US-00918585.
PR      06-AUG-2001; 2001US-00924419.
PR      13-AUG-2001; 2001US-00929404.
PR      16-AUG-2001; 2001US-00931836.
PR      28-AUG-2001; 2001US-00941992.
PR      29-AUG-2001; 2001WO-US027099.
PR      04-SEP-2001; 2001US-00946374.
PR      15-JAN-2002; 2002US-00052586.
```

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-332034/31.

P-PSDB; ASU86493.

Three hundred and five nucleic acids encoding PRO polypeptides, useful in
gene therapy, chromosome identification, tissue typing, and for detecting
the presence of tumor in a mammal.

Claim 2; Fig 601; 707pp; English.

The invention relates to three hundred and five nucleic acids encoding
PRO polypeptides (secreted and transmembrane), sequences 80% identical to
them, or encoding a PRO polypeptide lacking its associated signal peptide

or an extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide. Also included are the encoded PRO proteins, PRO expression vectors, host cells transformed with the vector (used to produce PRO proteins), a chimaeric molecule comprising the PRO polypeptide fused to a heterologous amino acid sequence, an anti-PRO antibody, a method for stimulating the release of tumor necrosis factor alpha (TNF-alpha) from human blood (by contacting the blood with PRO1079, PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567 or PRO3333), a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the cells with a PRO6029 polypeptide, a method for detecting the presence of tumor in a mammal and an oligonucleotide probe derived from any of the nucleotide sequences cited above. The PRO polypeptide or anti-PRO antibody is useful for preparing a medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful as hybridisation probes in chromosome and gene mapping, or in generating antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in assays to identify other proteins or molecules involved in a binding reaction, to generate transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides and nucleic acid molecules are also useful for detecting the presence of a tumour in a mammal, stimulating proliferation or differentiation of chondrocyte cells, stimulating the release of tumour necrosis factor-alpha from human blood, in gene therapy, or as molecular weight markers for protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. The present sequence is a cDNA encoding a PRO protein

SQ Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.3e-147 Length: 1841
Score: 1508.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-689-742-160 (1-280) x ACA73685 (1-1841)

QY 1 MetGlnAlaLysTyrSerThrArgAspMetLeuAspAspGlyAspThrThrMet 20
DB 144 ATGCGCCCAAGTACAGCAGCAGGAGCATGCTGGATGATGGGACACCAATG 203
QY 21 SerLeuHisSerGlnAlaSerAlaThrArgHisProGluProArgThrGluHis 40
DB 204 AGCCTGCATCTCAAGCCCTCTGCCAACCTCGGCATCCAGAGCCCGCGGCACAGAC 263
QY 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuVal 60
DB 264 AGGGCTCCCTCTCAACGTGGGACAGCAGTGGCCCTGACCTGCTGACTTTGTGTGTG 323
QY 61 LeuLeuLeuGlyLeuAlaAlaLeuGlyLeuLeuPheGlnTyrGlnLeuSerAsn 80
DB 324 CTGCTGATAGGCTGGCAGCCCTGGGGCTTTGTTTTTCAGTACTACCACTCTCCAAT 383
QY 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
DB 384 ACTGGTCAAGACACCACTTTCTCAATAGGAAGATTAGGAATACGTCCTCCAGAGTTG 443
QY 101 GlnSerLeuGlnValGlnAsnIleLeuValAlaGlySerLeuGlnHisValAlaGluLys 120
DB 444 CAATCTCTTCAAGTCAGAAATATAAGCTTTGAGGAAGTCTGAGATGTGGCTGAAAAA 503
QY 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
DB 504 CTCTGTCGTAGCTGTATACAAAGCTGGAGACACAGGTGAGCCCTGTGTACAGACAA 563
QY 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160

DB 564 TGGAAATGGCATGGAGACAAATTGGTACCAGTTCTATATAAGACAGCAAAAGTTGGGAGGAC 623
QY 161 CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
DB 624 TGTAAATATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAAACAACAAGAAGAC 683
QY 181 LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu 200
DB 684 CTGGAAATTTGCCGCTCTCAGAGCTACTCTGAGTTTCTTACTTTATTGGACAGGCTT 743
QY 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
DB 744 TTGCGCCCTGACAGTGGCAAGCCCTGGCTGGATGGATGGAAACCCCTTCTACTTCTGAA 803
QY 221 LeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAlaLeuLeu 240
DB 804 CTGTTCCATATTATATAGATGTCCAGGCCCAAGAGCAGAGACTGTGTGGCCATCTTC 863
QY 241 ArgGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
DB 864 AATGGATGATCTTCTCAAGGACTGCAAAAGAAATTGAAGCGTTGTCTGTGAGAGAGG 923
QY 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGlyAsp 280
DB 924 GCAGGATGGTGAAGCCAGAGAGCCCTCCATGTCCCCCTGAAACATTAGGCCAGGTGAC 983
RESULT 13
ACA06000
ID ACA06000 standard; cDNA; 1841 BP.
XX ACA06000;
XX
XX 29-MAY-2003 (first entry)
XX Human secreted/transmembrane protein (PRO) cDNA #301.
DE
XX
KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX
XX Homo sapiens.
XX
XX US2003036162-A1.
XX
PD 20-FEB-2003.
XX
PF 12-JUL-2002; 2002US-00194423.
XX
PR 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028551.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.

PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015284.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 29-AUG-2001; 2001WO-US027099.
PR 04-SEP-2001; 2001US-00946374.
PR 15-JAN-2002; 2002US-00052586.
XX PA (GETH) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-332039/31.
DR P-PSDB; ABU67706.

XX New secreted and transmembrane PRO polypeptides and nucleic acids, useful
PT in gene therapy, in chromosome and gene mapping, as chromosome markers,
PT in tissue typing, and in chromosome identification.

XX Claim 2; Fig 601; 706pp; English.

XX The invention discloses human nucleic acids encoding secreted and
CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that
CC specifically binds to the PRO polypeptide, a method for stimulating the
CC release of tumour necrosis factor alpha (TNF-alpha) from human blood by
CC contacting the blood a PRO polypeptide, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells by contacting the
CC cells with a PRO polypeptide, a method for detecting the presence of a
CC tumour in a mammal and an oligonucleotide probe derived from any of the
CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,
CC in chromosome and gene mapping, in generating antisense RNA and DNA, in
CC preparing PRO polypeptides by recombinant techniques and in gene therapy
CC (e.g. for replacement of defective gene). The PRO polypeptides are useful
CC as molecular weight markers for protein electrophoresis purposes, for
CC chromosome identification, as chromosome markers, as therapeutic agents,
CC for stimulating the release of TNF-alpha from human blood, for
CC stimulating the proliferation or differentiation of chondrocytes and
CC detecting the presence of a tumour. The PRO polypeptides and nucleic
CC acids may also be used diagnostically for tissue typing. The sequences

CC presented in ACA05700-ACA06004 are the cDNAs encoding the PRO
CC polypeptides of the invention
XX
SQ Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3,3e-147	Length:	1841
Score:	1508.00	Matches:	280
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-10-689-742-160 (1-280) x ACA06000 (1-1841)

Qy	1	MetGlnAlaIysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMet	20
Db	144	ATGCAGGCCAAGTACAGCAGCAGGAGCATGTGGATGATGATGGGACACCAACATG	203
Qy	21	SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis	40
Db	204	AGCTGCAATTCCTCAAGCTCTGCCCACTCGGCATCCAGAGCCCGGCGCAGAGGCAC	263
Qy	41	ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal	60
Db	264	AGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCTGCTGCTGCTGCTGCTG	323
Qy	61	LeuLeuIleGlyLeuAlaAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsn	80
Db	324	CTGCTGATAGGCTGGCAGCCCTGGGGCTTTTGTGTTTTCAGTACTACACAGCTCTCCAAT	383
Qy	81	ThrGlyGlnAspThrIleSerGlnMetGluGlnArgLeuGlyAsnThrSerGlnGluLeu	100
Db	384	ACTGGTCAAGACACCAATTTCTCAATGGAAGAAGATTAGGAATACCTCCAGAGTTG	443
Qy	101	GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys	120
Db	444	CAATCTCTTCAAGTCCAGAAATATAAAGCTTCAGAGAGCTGCAGCATGTGGCTGAAAAA	503
Qy	121	LeuCysArgGluLeuTyrAsnIleAlaGlyAlaHisArgCysSerProCysThrGluGln	140
Db	504	CTCTGCTGAGCTGTATACAAAGCTGGAGCACACAGTGCAGCCCTTGTACAGAACAA	563
Qy	141	TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp	160
Db	564	TGGAATGGCATGGAGCAATTTGTCACAGTTCTATAAAGACAGACAAAGTTGGAGGAC	623
Qy	161	CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp	180
Db	624	TGTAATATTTCCTGCTTAGTGAAACTCTACCATGCTGAAGATAAACAACAAGAGAC	683
Qy	181	LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu	200
Db	684	CTGGAATTTGCCGCTCTCAGAGCTACTCTCAGATTTTCTACTCTCTATTATGACAGGGTT	743
Qy	201	LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu	220
Db	744	TTGGCCCTGACAGTGGCAGGCTGGCTGGATGGATGGAAACCCCTTTTCACTTCTGAA	803
Qy	221	LeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu	240
Db	804	CTGTTCCATATTATAATAGATGTCAACAGCCCAAGACAGACAGCTGTGTGGCCATCCTC	863
Qy	241	AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg	260
Db	864	AATGGATGATCTCTCTCAAGAGCTGCAAGAAATGAACGCTGTGTCTGTGAGAGAGG	923
Qy	261	AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyLysGlyAsp	280
Db	924	CGAGGATGGTGAAGCCAGAGAGCTCCATGTCCCCCTGAAACATTAGGCGCAAGGTGAC	983

RESULT 14
ACA66834

PR 28-FEB-2001; 2001WO-US006520.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 28-AUG-2001; 2001US-00941992.
 XX (GETH) GENENTECH INC.
 PA
 XX
 PI Ashtkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 XX WPI; 2003-352829/33.
 DR P-PSDB; ABU72542.
 XX
 PT New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
 PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's
 PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
 PT disease.
 XX
 PS Claim 1; Fig 229; 663pp; English.
 PS
 CC The invention describes a new isolated nucleic acid molecule comprising
 CC the full length coding sequence of the DNA deposited with the American
 CC Type Culture Collection (e.g. ATCC deposit No. 209621, 552-PTA, 819-PTA,
 CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA
 CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
 CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
 CC are particularly useful for detecting or treating e.g. malignancies or
 CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
 CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's
 CC disease in mammals. The PRO polypeptides are useful in drug screening,
 CC particularly as targets for therapeutic intervention in these diseases,
 CC and in the diagnostic determination of the presence of these diseases.
 CC The PRO polypeptides are also useful as molecular weight markers, or for
 CC chromosome identification. The PRO genes are useful as hybridisation
 CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
 CC The PRO genes may also be used in gene therapy, particularly for
 CC replacing a defective gene. This sequence encodes a novel human secreted
 CC and transmembrane PRO polypeptide
 XX
 SQ Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;

 Alignment Scores:
 Pred. No.: 3.3e-147 Length: 1841
 Score: 1508.00 Matches: 280
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

 US-10-689-742-160 (1-280) x ACA64371 (1-1841)

 QY 1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspGlyAspThrThrMet 20
 DB 144 ATGCAGGCCCAAGTACAGCAGCAGCAGGAGCATGCTGGATGATGATGGGACACCACTG 203

 QY 21 SerLeuHisSerGlnAlaSerAlaThrArgHisProGluProArgArgThrGluHis 40
 DB 204 AGCCGTGCATTCCTCAAGCCCTCTCCCACTCCGCGATCCAGAGCCCGCGGCACAGAGC 263

 QY 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal 60
 DB 264 AGGGCTCCCTCTTCAACGTGGCGACCAAGTGGCCCTGACCTGCTGACTTGTGTGGTG 323

 QY 61 LeuLeuIleGlyLeuAlaAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsn 80
 DB 324 CTGCTGATAGGGCTGGAGCCCTGGGGCTTTTGTGTTTTCAGTACTACCACTCTCCAA 383

 QY 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnLeuLeu 100

 DB 384 ACTGTCAGACACCACTTCTCAATGGAGAAAGATTAGGAAATACGTCCTCCAGAGTTG 443
 QY 101 GlnSerLeuGlnValGlnAsnIleLeuAlaGlySerLeuGlnHisValAlaGluLys 120
 DB 444 CAATCTCTTCAAGTCCAGAAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAA 503

 QY 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
 DB 504 CTCTGTGCGAGCTGTATAACAAAGCTGGAGCACACAGGTGAGCCCTTGTACAGAACAA 563

 QY 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
 DB 564 TGGAAATGGCATGGAGACAAATTGCTACCAAGTTCTATTAAGACAGCAAAAGTTGGGAGG 623

 QY 161 CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
 DB 624 TGTAAATATTTCTGCTTAGTGAAAACTCTACCATGCTGAAGATAAAACAACAAGAAGAC 683

 QY 181 LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu 200
 DB 684 CTGGAAATGGCGCGCTCTCAGAGCTACTCTGAGTTTCTCTCTTATTGGACAGGCTT 743

 QY 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
 DB 744 TTGCGCCCTGACAGTGGCAAGCCCTGGCTGTGGATGGATGGAAACCCCTTCTACTTCTGAA 803

 QY 221 LeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu 240
 DB 804 CTGTTCCATATTTATTAATAGATGTCCACAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTC 863

 QY 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
 DB 864 AATGGATGATCTCTCTCAAGGACTGCAAGAAGAAATTTGAAGCGTGTGTCTGTGAGAGAGG 923

 QY 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGlyAsp 280
 DB 924 GCAGGAATGGTGAAGCCAGAGAGCCCTCCATGTCCCCCTGAAACATATTAGGCCAGGTGAC 983

Search completed: October 8, 2005, 01:10:59
 Job time : 563.659 secs

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LQVONIKLAGSLQVHAEKLCRELANKAGHRCSPCTEOMKWHGNCQFYKDSKSWED
CKYCLSENSTMLKINKQEDLEPAASQSYSEFFYSYWTGLLRPPSGKANLWMDGTPTT
SELPHIIDIIVSPRSRDCVAILNGMIFSKCKELKRCVCERRAGWVPSUHVPPETL
GEGD"

ORIGIN

Alignment Scores:
Pred. No.: 6,79e-147 Length: 1756
Score: 1508.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-689-742-160 (1-280) x CQ783156 (1-1756)

Qy 1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspGlyAspThrThrMet 20
Db 64 ATGCAGGCCAAGTACAGCAGCAGGAGGACATGCTGGATGATGATGGGACACACCATG 123

Qy 21 SerLeuHisSerGlnAlaSerAlaThrArgHisProGluProArgArgThrGluHis 40
Db 124 AGCCTGCAATTCCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCGCGCACAGAGCAC 183

Qy 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuVal 60
Db 184 AGGGCTCCCTCTTCAACGTGGCGACCATGGCCCTGACCTTGCTGTGCTTGTGTTG 243

Qy 61 LeuLeuIleGlyLeuAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsn 80
Db 244 CTGCTGTAGAGGCTGGCAGCCCTGGGCTTTGTTTTTCAGTACTACCACTCTCCAA 303

Qy 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
Db 304 ACTGGTCAAGACACCATTTCTCAATGGAAGAAAGATTAGGAAATACCTCCCAAGAGTTG 363

Qy 101 GlnSerLeuGlnValGlnAsnIleLeuAlaGlySerLeuGlnHisValAlaGluLys 120
Db 364 CAATCTCTTCAAGTCCAGATATAAGCTTGCGAGNAGTCTGCAGCATGTGCTGGAANA 423

Qy 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
Db 424 CTCTGTCTGAGCTGTATACAAAGCTGGAGCACACAGCTGCAGCCCTTGTACAGAACAA 483

Qy 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
Db 484 TGGAAATGGCATGGAGACAAATTTGCTTACCAAGTTCTATAAAGACAGCAAAAGTTGGAGGAC 543

Qy 161 CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
Db 544 TGTAAATATTTCTGCCTTAGTGAAACCTCTACCATGCTGAAGATATAACAAAGAACAC 603

Qy 181 LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu 200
Db 604 CTGGAATTTGGCGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATGGACAGGCTT 663

Qy 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
Db 664 TTGGCCCTTGACAGTGGCAAGCCCTGGCTGGATGGATGGAACCCCTTTCACTTCTGAA 723

Qy 221 LeuPheHisIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu 240
Db 724 CTGTTTCCATATTAATATAGATGTACACAGCCCAAGAGCAGAGACTGTGTGGCCATCTT 783

Qy 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
Db 784 AATGGATGATCTTCTCAAGGACTGCAAGAGATTGAAGCGTTGTGTGTGAGAGAGG 843

Qy 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280
Db 844 GCAGGAATGGTGAAGCCAGAGAGCCTCCATGTGTCCTCCCTGAAACATTAGGCGAAGGTGAC 903

RESULT 2

BD127503 1756 bp DNA linear PAT 18-SEP-2002
LOCUS Primer for synthesizing full-length cDNA and use thereof.
DEFINITION BD127503
ACCESSION BD127503
VERSION BD127503.1 GI:23222448
KEYWORDS JP 2002017375-A/2934.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (Bases 1 to 1756)
AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002017375-A 2934 22-JAN-2002;
COMMENT HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/2934
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
PI ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10,
PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof PH Key
FT CDS Location/Qualifiers
source 1..1756
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Pred. No.: 6,79e-147 Length: 1756
Score: 1508.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-689-742-160 (1-280) x BD127503 (1-1756)

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Qy 21 SerLeuHisSerGlnAlaSerAlaThrArgHisProGluProArgArgThrGluHis 40
Db 124 AGCCTGCAATTCCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCGCGCACAGAGCAC 183

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Qy 61 LeuLeuIleGlyLeuAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsn 80
Db 244 CTGCTGTAGAGGCTGGCAGCCCTGGGCTTTGTTTTTCAGTACTACCACTCTCCAA 303

Qy 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
Db 304 ACTGGTCAAGACACCATTTCTCAATGGAAGAAAGATTAGGAAATACCTCCCAAGAGTTG 363

Qy 101 GlnSerLeuGlnValGlnAsnIleLeuAlaGlySerLeuGlnHisValAlaGluLys 120

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QY      141  TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
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QY      161  CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
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Db      604  CTGGAATTTGCCGCTGCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGCTT 663
QY      201  LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
Db      664  TTGCGCCCTTCAGATGGCAAGCCCTGGCTGGATGGATGGAACCCCTTTCACTTCTGAA 723
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QY      241  AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
Db      784  AATGGGATGATCTTCTCAAGAGACTGCAAGAAATGAAGCGTTGTCTGTGAGAGAGG 843
QY      261  AlaGlyMetValLysProGluSerLeuHisValProGluThrLeuGlyGluGlyAsp 280
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ACCESSION AK075114.1 GI:22760991
VERSION    AK075114.1
KEYWORDS   oligo capping; fis (full insert sequence).
SOURCE     Homo sapiens
           Organism: human
REFERENCE  1
AUTHORS    Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
           Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
           Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
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           Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
           Ninomiya,K.
           NEDO human cDNA sequencing project
TITLE      Unpublished
JOURNAL    2 (bases 1 to 1756)
REFERENCE  Isogai,T. and Otsuki,T.
AUTHORS    Direct Submission
TITLE      Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
           Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
           (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
           NEDO human cDNA sequencing project supported by Ministry of
           Economy, Trade and Industry of Japan; cDNA full insert sequencing:
           Research Association for Biotechnology; cDNA library construction:
           Institute of Medical Science, University of Tokyo, Laboratory of
           Genome Structure, Human Genome Center; cDNA 5'- and 3'-end one pass
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CDS
ORIGIN
Alignment Scores:
Pred. No.:      6,79e-147      Length:      1756
Score:          1508.00        Matches:    280
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    100.00%       Indels:       0
DB:              9              Gaps:       0

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QY      41  ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal 60
Db      184  AGGGCTCCCTCTTCAACGTGGCGCAGCAGTGGCCCTGACCTCTGTGCTTTGTGCTGGTG 243
QY      61  LeuLeuLeuGlyLeuAlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsn 80
Db      244  CTGCTGTAGAGGCTGGCAGCCCTGGGCTTTGTTTTTTCAGTACTACCACTCTCCAT 303
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Db      304  ACTGGTCAAGACACCACTTCTCAATGGAAGAAAGATTAGGAAATACGTCCTCAAGAGTTG 363
QY      101  GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120
Db      364  CAATCTCTTCAAGTCCAGAAATATAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAA 423
QY      121  LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
Db      424  CTCTGTGCTGAGCTGTATACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAA 483
QY      141  TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
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QY      161  CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
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Db      664  TTGCGCCCTTCAGATGGCAAGCCCTGGCTGGATGGATGGAACCCCTTTCACTTCTGAA 723
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ACCESSION  BD074859
VERSION    BD074859.1 GI:22620462
KEYWORDS  JP 2001515717-A/1.
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 1776)
AUTHORS   Jacoby,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Evans,C.,
          Metberg,D., Treacy,M., Agostino,M.J. and Spaulding,V.
TITLE     Secreted proteins and polynucleotide encoding the same
JOURNAL   Patent: JP 2001515717-A 1 25-SEP-2001;
          GENETICS INSTITUTE INC
COMMENT   OS Homo sapiens (human)
          FN JP 2001515717-A/1
          PD 25-SEP-2001
          PF 08-SEP-1998 JP 2000510854
          PR 08-SEP-1997 US 08/929007
          PI KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE,PI
          PI CHERYL EVANS,
          PI DAVID MERBERG,MAURICE TREACY,MICHAEL J AGOSTINO,VIKKI PI
          SPAULDING
          PC C12N15/09,A61K38/00,A61K38/00,A61P43/00,C07K14/52,C12N1/21,PC
          C12N5/10,
          PC C12N15/00,A61K37/02,A61K37/18,C12N5/00
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ORIGIN
Alignment Scores:
Pred. No.: 6.89e-147 Length: 1776
Score: 1508.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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LOCUS      AR252588
DEFINITION Sequence 318 from patent US 6478825.
ACCESSION  AR252588
VERSION    AR252588.1 GI:27300496
KEYWORDS  .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 1841)
AUTHORS   Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE     Implant, method of making same and use of the implant for the
          treatment of bone defects.
JOURNAL   Patent: US 6478825-A 318 12-NOV-2002;
FEATURES   Location/Qualifiers
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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DB	264 AGGGCTCCCTCTTCAAGTGGGACCAAGTGGCCCTGACCTGCTGACTTTGTGCTTGGTG 323
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DEFINITION	Sequence 457 from patent US 6725730.
ACCESSION	AR528680
VERSION	AR528680.1 GI:53916758
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 1841)
AUTHORS	Bollinger, C.L. Jr.
TITLE	Crane test weight assembly and method
JOURNAL	Patent: US 6725730-A 457 27-APR-2004;
FEATURES	Location/Qualifiers
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DB	864 AATGGATGATCTTCTCAAGGACTGCAAGAAATTTGAAGCGTTGTCTGTGAGAGAGG 923
QY	261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluArg 280
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LOCUS AX055702 1841 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 17 from Patent WO0073348.
ACCESSION AX055702
VERSION AX055702.1 GI:12228834
KEYWORDS Homo sapiens (human)
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Baker, K.P., Goddard, A., Gurney, A.L., Hebert, C., Henzel, W.,
Karakoff, R.C., Shelton, D.L., Smith, V., Watanabe, C.K. and Wood, W.I.
TITLE Methods and compositions for inhibiting neoplastic cell growth
JOURNAL Patent: WO 0073348-A 17 07-DEC-2000;
Genentech, Inc. (US)

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Alignment Scores:
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Percent Similarity: 100.00% Conservative: 0
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DB: 6 Gaps: 0

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DB 504 CTCTGCTGAGCTGTATACAAAGCTGAGACACAGTGGCGCCCTTGTACAGAACAA 563
QY 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
DB 564 TGGAAATGGCATGGAGACAATTTGCTACCATTTCTATAAAGACAGCAAAAGTTGGGAGAC 623
QY 161 CysLysTyrPheCysLeuSerGlnAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
DB 624 TGTAATAATTTCTGCTTAGTGAAAACTCTACCATGCTGAAGATAAACAAACAAGAC 683
QY 181 LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGluLeu 200
DB 684 CTGGAAATTTGCCCGTCTCAGAGCTACTCTGAGTTTCTTACTCTATTGAGCAGGGTT 743
QY 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220

DB 744 TTGGCCCTGACAGTGGCAAGCCCTGGCTGGATGGATGGAAACCCCTTTCATTCTGAA 803
QY 221 LeuPheHisIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 240
DB 804 CTGTTCCCATATTATTAATAGATGTACCAGCCCAAGAGCAGAGACTGTGTGGCCATCTTC 863
QY 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
DB 864 AATGGATGATCTTCTCAAGGACTGCAAGAAATTGAAGCGTTGTGTCTGTGAGAGAGG 923
QY 261 AlaGlyMetValLysProGluSerLeuHisValProGluThrLeuGlyGluGlyAsp 280
DB 924 GCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGAC 983
RESULT 8
AX376534
LOCUS AX376534 1841 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 601 from Patent WO0168848.
ACCESSION AX376534
VERSION AX376534.1 GI:19170655
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 601 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
source
1..1841
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 7,228-147 Length: 1841
Score: 1508.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-689-742-160 (1-280) x AX376534 (1-1841)

QY 1 MetGlnAlaLysTyrSerThrArgAspMetLeuAspAspGlyAspThrThrMet 20
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QY 21 SerLeuHisSerGlnAlaSerAlaThrArgHisProGluProArgThrGluHis 40
DB 204 AGCCTGTCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCGCGCACACAGAC 263
QY 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuThrLeuThrLeuVal 60
DB 264 AGGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCTGCTGCTGCTGGTG 323
QY 61 LeuLeuLeuLeuLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuSerAsn 80
DB 324 CTGCTGATAGGCTGGCGCCCTGGGGCTTTTGTGTTTTCAGTACTACAGCTCTCCAA 383
QY 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
DB 384 ACTGTCGAAGACACCATTTCTCAATGGAAGAAAGATTAGGAATACGTCCCAAGATTG 443
QY 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120

Db 444 CAATCTCTTCAAGTCAGATATAAAGCTTGAGGAGTCTGCAGCATGTGCGTGA AAA 503
 QY 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
 Db 504 CTCTGTGCTGAGCTGTATACAAAGCTGGAGCACACAGGTGAGCCCTTGTACAGAA CA 563
 QY 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
 Db 564 TGGAAATGGCATGGAGACAATTTGCTACCAAGTCTATAAAGACAGCAAAAGTTGGAGGAC 623
 QY 161 CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
 Db 624 TGTAAATATTTTCTGCTTAGTGAAGTCTACCATGCTGAAGTAAACAAACAAGAGAC 683
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 Db 744 TTGCGCCCTGACAGTGGCAAGCCCTGGCTGTGGATGGATGGAACCCCTTTCTACTTCTGAA 803
 QY 221 LeuPheHisIleIleAspValThrSerProArgSerArgAspCysValAlaLalleLeu 240
 Db 804 CTGTTCCATATTTATATAGATGTCCACGCCCAAGAGCAGAGACTGTGTGGCCATCTCTC 863
 QY 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
 Db 864 AATGGAGTATCTTCTCAAGGACTGCAAGAAGATTGAAGCGTTGTGTGTGAGAGAGG 923
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 Db 924 CGAGGAATGGTGAAGCCAGAGAGCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGAC 983

RESULT 9

AX403431
 LOCUS AX403431 1841 bp DNA linear PAT 14-JUN-2002
 DEFINITION Sequence 318 from Patent WO0073454.
 ACCESSION AX403431
 VERSION AX403431.1 GI:21436942

KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Ashkenazi, A.J., Baker, K.P., Botstein, D., Deanovers, L., Eaton, D., Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P., Grimaldi, C.J., Gurney, A.L., Kijavins, I., Napier, M.A., Pan, J., Paoni, N.F., Roy, M., Stewart, T.A., Tamas, D., Watanabe, C.K., Williams, P., Wood, W.I. and Zhang, Z.
 1 Secreted and transmembrane polypeptides and nucleic acids encoding the same

TITLE
 JOURNAL Patent: WO 0073454-A 318 07-DEC-2000;
 Genentech Inc. (US)
 FEATURES
 source Location/Qualifiers
 1..1841
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
 Alignment Scores: 7.22e-147 Length: 1841
 Pred. No.: 1508.00 Matches: 280
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 100.00% Gaps: 0
 DB: 6

US-10-689-742-160 (1-280) x AX403431 (1-1841)
 QY 1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspGlyAspThrThrMet 20

Db 144 ATGAGGCCCAAGTACAGCAGACGAGGACATGCTGGATGATGGGACACCCATG 203
 QY 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40
 Db 204 AGCGTCCATTTCTCAAGCCCTCTGCCACACTCGGCATCCAGAGCCCGGCGCAGAGCAC 263
 QY 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal 60
 Db 264 AGGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCCCTGCTGACTTTGTCTTGGTG 323
 QY 61 LeuLeuIleGlyLeuAlaAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsn 80
 Db 324 CTGCTGATAGGCTGGCAGCCCTGGGGCTTTTGTGTTTTTCAGTACTTACCAGCTCTCCAAT 383
 QY 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
 Db 384 ACTGCTCAAGACACCATTTCTCAATGGAAGAAGATTAGGAATACGTCCTCAAGAGTTG 443
 QY 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120
 Db 444 CAATCTCTTCAAGTCCAGATATAAAGCTTGCAAGAGTCTGCAGCATGTGGCTGAAAAA 503
 QY 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
 Db 504 CTCTGTGCTGAGCTGTATAAAGCTGGAGCACACAGGTGAGCCCTTGTACAGAACAA 563
 QY 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
 Db 564 TGGAAATGGCATGGAGACAATTTGCTACCATGCTTATTAAGACAGCAAAAGTTGGAGGAC 623
 QY 161 CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
 Db 624 TGTAAATATTTCTGCTTAGTGAAGTCTACCATGCTGAAGTAAACAAACAAGAGGAC 683
 QY 181 LeuGluPheAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu 200
 Db 684 CTGGAAATTTGCGCGCTCTCAGAGTACTCTGAGTTTCTACTCTTATTGGACAGGGCTT 743
 QY 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
 Db 744 TTGCGCCCTGACAGTGGCAAGCCCTGGCTGTGGATGGATGGAACCCCTTTCTACTTCTGAA 803
 QY 221 LeuPheHisIleIleAspValThrSerProArgSerArgAspCysValAlaLalleLeu 240
 Db 804 CTGTTCCATATTTATATAGATGTCCACGCCCAAGAGCAGAGACTGTGTGGCCATCTCTC 863
 QY 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
 Db 864 AATGGAGTATCTTCTCAAGGACTGCAAGAAGATTGAAGCGTTGTGTGTGAGAGAGG 923
 QY 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280
 Db 924 CGAGGAATGGTGAAGCCAGAGAGCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGAC 983

RESULT 10
 LOCUS AX454580 1841 bp DNA linear PAT 06-JUL-2002
 DEFINITION Sequence 165 from Patent WO0208284.
 ACCESSION AX454580
 VERSION AX454580.1 GI:21713914

KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P., Gurney, A.L., Hillan, C.K., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.
 1 Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis

TITLE
 Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis

JOURNAL

Patent: WO 0208284-A 165 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillman, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)

FEATURES

Location/Qualifiers

1..1841
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 7,22e-147 Length: 1841
Score: 1508.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-689-742-160 (1-280) x AX454580 (1-1841)

Qy 1 MetGlnAlaLysTyrSerThrArgAspMetLeuAspAspGlyAspThrThrMet 20
Db 144 ATGCAGGCCAAGTACAGCAGCAGGACATCTGGATGATGATGGGACACACCATG 203
Qy 21 SerLeuHisSerGlnAlaSerAlaThrArgHisProGluProArgArgThrGluHis 40
Db 204 AGCCTGCATTTCTCAAGCCTCTGCCACAACTGGCATCCAGAGCCCGCGGCACAGAGC 263
Qy 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuThrLeuThrLeuVal 60
Db 264 AGGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCTGTGCTGTGGTG 323
Qy 61 LeuLeuIleGlyLeuAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsn 80
Db 324 CTGCTGATAGGGCTGGAGCCCTGGGGCTTTGTTTTTTCAGTACTACAGCTCTCCAA 383
Qy 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
Db 384 ACTGCTCAAGACACCATTTCTCAATGGAAGAGATTAGGAAATACGTCACCAAGATTG 443
Qy 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValaGluLys 120
Db 444 CAATCTCTTCAAGTCCAGATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAA 503
Qy 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
Db 504 CTCTGCTGAGCTGTATTAACAAAGCTGGAGCAGACAGGTGGAGCCCTTGTACAGAA 563
Qy 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
Db 564 TGGAAATGGCATGGAGACAATTTGCTACCAAGTCTTATAAAGCAGCAAAAGTTGGGAG 623
Qy 161 CysLysTyrPheCysLeuSerGlnAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
Db 624 TGTAAATATTTCTGCTTTAGTGAAACCTCTACCATGCTGAAGATATAAACAAGAGAC 683
Qy 181 LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu 200
Db 684 CTGGNAATTTGGCGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTATTTGACAGGGCT 743
Qy 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
Db 744 TTGCGCCCTGACAGTGGCAAGCCCTGGCTGTGATGATGGAACCCCTTTCACTTCTGAA 803
Qy 221 LeuPheHisIleIleAspValThrSerProArgSerArgAspCysValaIleLeu 240
Db 804 CTGTTCCATATTATAATAGATGTACCAGCCCAAGAGACAGAGACTGTGTGGCCATCTCT 863

Qy 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
Db 864 AATGGGATGATCTTCTCAAGGACTGCAAGAGATTGAAGCGTTGTCTGTGAGAGAG 923
Qy 261 AlaGlyMetValLysProGluSerLeuHisValProGluThrLeuGlyGluGlyAsp 280
Db 924 GCAGGAATGGTGAAGCCAGAGAGCCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGAC 983

RESULT 11

AX464324 LOCUS 1841 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 457 from Patent WO0140466.
ACCESSION AX464324
VERSION AX464324.1 GI:21899178
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Beresini, M., Deforge, L., Desnovers, L., Filvaroff, E.,
Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.L. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 457 07-JUN-2001;
Genentech Inc. (US)
FEATURES
Location/Qualifiers
source 1..1841
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 7,22e-147 Length: 1841
Score: 1508.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-689-742-160 (1-280) x AX464324 (1-1841)

Qy 1 MetGlnAlaLysTyrSerThrArgAspMetLeuAspAspGlyAspThrThrMet 20
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Qy 21 SerLeuHisSerGlnAlaSerAlaThrArgHisProGluProArgArgThrGluHis 40
Db 204 AGCCTGCATTTCTCAAGCCTCTGCCACAACTGGCATCCAGAGCCCGCGGCACAGAGC 263
Qy 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuThrLeuThrLeuVal 60
Db 264 AGGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCTGTGCTGTGGTG 323
Qy 61 LeuLeuIleGlyLeuAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsn 80
Db 324 CTGCTGATAGGGCTGGCAGCCCTGGGGCTTTGTTTTTTCAGTACTACAGCTCTCCAA 383
Qy 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
Db 384 ACTGCTCAAGACACCATTTCTCAATGGAAGAGATTAGGAAATACGTCACCAAGATTG 443
Qy 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValaGluLys 120
Db 444 CAATCTCTTCAAGTCCAGATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAA 503
Qy 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
Db 504 CTCTGCTGAGCTGTATTAACAAAGCTGGAGCAGACAGGTGGAGCCCTTGTACAGAA 563

QY 141 TtpLysTrpHisGlyAspAsnCysTrpGlnPheTrpLysAspSerLysSerTrpGluAsp 160
 DB 564 TGGAAATGGCATGGAGACAAATGCTACCAAGTTCTATAAGACAGACAAAGATTGGAGGAC 623
 QY 161 CysLysTrpPheCysLysSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
 DB 624 TGTAAATATTCTGCTTGTAGTGAATACTTACCAATCTGAGATTAATGGAAGAGAC 683
 QY 181 LeuGluPheAlaAlaSerGlnSerTrpSerGluPhePheTrpTrpThrGlyLeu 200
 DB 684 CTGGAATTTGCGCGCTCTCAGAGTACTCTGAGTTTCTTACTTTATTTGGACAGGCTT 743
 QY 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
 DB 744 TTGGCCCTTGACAGTGGCAAGGCTGGCTGTGATGGATGGACCCCTTTTCACTTCTGAA 803
 QY 221 LeuPheHisIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu 240
 DB 804 CTGTTCCATATTATATAGATGTACCAAGCAAGAGCAGAGACTGTGTGGCCATCTCTC 863
 QY 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
 DB 864 AATGGGATGATCTTCTCAAGGACTGCAAGGAATTGAAGCGTTGTCTGTGAGAGAGG 923
 QY 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280
 DB 924 GCAGGAATGGTGAAGCCAGAGAGCCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGAC 983

RESULT 12

AX491058 1841 bp DNA linear PAT 16-AUG-2002
 LOCUS Sequence 165 from Patent WO0200690.
 DEFINITION AX491058
 ACCESSION AX491058.1 GI:22323866
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS

Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
 Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
 and Ye, W.
 TITLE Compositions and methods for the diagnosis and treatment of
 disorders involving angiogenesis
 JOURNAL Patent: WO 0200690-A 165 03-JAN-2002;
 Genentech, Inc. (US)

FEATURES

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 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
 Pred. No.: 7,22e-147 Length: 1841
 Score: 1508.00 Matches: 280
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-689-742-160 (1-280) x AX491058 (1-1841)

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QY 21 SerLeuHisSerGlnAlaSerAlaThrArgHisProGluProArgArgThrGluHis 40

DB 204 AGCTGCAATTTCTCAAGCGCTCTGCCCAACTCGGCATCCAGAGCCCGCGCAGAGCAC 263

QY 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal 60
 DB 264 AGGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCTGCTGACTTTGTGCTTGGTG 323
 QY 61 LeuLeuIleGlyLeuAlaLeuGlyLeuLeuPhePheGlnTrpTrpGlnLeuSerAsn 80
 DB 324 CTGCTGATAGGCTGGCAGCCCTGGGGCTTTTGTGTTTTTTCAGTACTACCAAGCTTCCAAT 383
 QY 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
 DB 384 ACTGGTCAAGACACCATTTCTCAATGGAAGAAAGATTAGGAAATACGTCCTCCCAAGAGTTG 443
 QY 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120
 DB 444 CAATCTCTTCAAGTCAGAATATAAAGCTTGCAGAAAGTCTGCAGCATGTGGCTGAAAAA 503
 QY 121 LeuCysArgGluLeuTrpAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
 DB 504 CTCTGCTGAGCTGTATACCAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGACAA 563
 QY 141 TrpLysTrpHisGlyAspAsnCysTrpGlnPheTrpLysAspSerLysSerTrpGluAsp 160
 DB 564 TGGAAATGGCATGGAGACAAATGCTTACCAAGTCTATAAAGACAGCAAAAGTTGGGAGGAC 623
 QY 161 CysLysTrpPheCysLysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
 DB 624 TGTAAATATTCTTGGCTTTAGTGAATACTTACCATGTGAAAGATTAACAAACAGAGAC 683
 QY 181 LeuGluPheAlaAlaSerGlnSerTrpSerGluPhePheTrpTrpThrGlyLeu 200
 DB 684 CTGGAATTTGCGCGCTCTCAGAGTACTCTGAGTTTCTTACTTATTTGGACAGGCTT 743
 QY 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
 DB 744 TTGGCCCTTGACAGTGGCAAGGCTGGCTGTGATGGATGGACCCCTTTTCACTTCTGAA 803
 QY 221 LeuPheHisIleIleLysValThrSerProArgSerArgAspCysValAlaIleLeu 240
 DB 804 CTGTTCCATATTATATAGATGTACCAAGCAAGAGCAGAGACTGTGTGGCCATCTCTC 863
 QY 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
 DB 864 AATGGGATGATCTTCTCAAGGACTGCAAGGAATTGAAGCGTTGTCTGTGAGAGAGG 923
 QY 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280
 DB 924 GCAGGAATGGTGAAGCCAGAGAGCCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGAC 983

RESULT 13

AY358587 1841 bp mRNA linear PRI 03-OCT-2003
 LOCUS Homo sapiens clone DNAS9777 QAKY569 (U9569) mRNA, complete cds.
 DEFINITION AY358587
 ACCESSION AY358587
 VERSION AY358587.1 GI:37182295
 KEYWORDS
 SOURCE FLI CDNA.
 ORGANISM Homo sapiens

REFERENCE 1 (Bases 1 to 1841)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS

Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
 Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
 Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E.,
 Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,
 Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,
 Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,
 Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wleand, D., Woods, K.,
 Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
 Goddard, A., Wood, W.I. and Godowski, P.

TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:
 A Bioinformatics Assessment

JOURNAL Genome Res. 13 (10), 2265-2270 (2003)

PUBMED 12975309
REFERENCE 2 (bases 1 to 1841)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES
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ORIGIN
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Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-689-742-160 (1-280) x AY358587 (1-1841)

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Qy 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuVal 60
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Qy 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
Db 384 ACTGGTCAAGACACCATTTCTCAATGGAAGAGATGAGGAATACGCTCCAGAGTTG 443
Qy 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGlyLys 120
Db 444 CAATCTCTTCAAGTCCAGATATAAAGCTTCGAGGAAGCTTCGAGGAGTGTGGCTGMAAAA 503
Qy 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
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ACCESSION BC067746
VERSION BC067746
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2701)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heideh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshitoki,S.,
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Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzyzanski,M.I., Skalska,U., Smalus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2701)
Strausberg,R.
Direct Submission
Submitted (19-MAR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapsb-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael Brownstein / Ted Usdin
Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www.ehgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 168 Row: k Column: 9
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23503320.

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 GEGD"

ORIGIN

Alignment Scores:

Pred. No.: 1,19e-146 Length: 2701
 Score: 1508.00 Matches: 280
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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US-10-689-742-160 (1-280) x BC067746 (1-2701)

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DB 364 CAATCTCTTCAAGTCCAGATATAAAGCTTGCAGGAAGTCTCCAGCATGTGCTGAAAAA 423
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 BC039072
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 ACCESSION BC039072
 VERSION BC039072.1 GI:24660225
 KEYWORDS MGC.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 1797)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Rana, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalilus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., Skalska, U., Marra, M.A.
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 1797)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (01-NOV-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amgobcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulaeeged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 51 Row: 0 Column: 12
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7706062.

FEATURES

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ORIGIN

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US-10-689-742-160 (1-280) x BC039072 (1-1797)

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Job time : 4265.3 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 8, 2005, 00:39:18 ; Search time 198.068 Seconds
(without alignments)
2313.130 Million cell updates/sec

Title: US-10-689-742-160
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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
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Searched: 1202784 seqs, 818138359 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	355.5	23.6	970	4	US-09-016-434-800
6	351.5	23.3	1737	4	US-09-482-273-34
7	308.5	20.5	1897	2	US-08-809-494A-1
8	308.5	20.5	1897	3	US-09-352-302-1
9	308.5	20.5	1906	2	US-08-809-494A-3
10	308.5	20.5	1906	3	US-09-352-302-3
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12	301.5	20.0	1318	3	US-09-352-302-5

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15	251	16.6	990	2	US-08-688-342-2	Sequence 2, Appli
16	251	16.6	990	2	US-09-113-788-2	Sequence 2, Appli
17	251	16.6	990	4	US-09-016-434-804	Sequence 804, App
18	250	16.6	1092	4	US-09-898-554-19	Sequence 19, Appli
19	248.5	16.5	505	4	US-09-976-594-1045	Sequence 1045, Ap
20	245	16.2	721	4	US-09-898-554-28	Sequence 28, Appli
21	225.5	15.0	1192	4	US-09-898-554-12	Sequence 12, Appli
22	224	14.9	606	4	US-09-898-554-15	Sequence 15, Appli
23	223	14.8	1092	4	US-09-898-554-11	Sequence 11, Appli
24	221	14.7	744	4	US-09-898-554-13	Sequence 13, Appli
25	215	14.3	1241	4	US-09-949-016-2943	Sequence 2943, Ap
26	205.5	13.6	468	4	US-09-898-554-17	Sequence 17, Appli
27	203	13.5	871	1	US-08-650-578-1	Sequence 1, Appli
28	203	13.5	1364	4	US-09-949-016-329	Sequence 329, App
29	202	13.4	763	4	US-09-919-039-129	Sequence 129, App
30	200.5	13.3	621	4	US-09-898-554-25	Sequence 25, Appli
31	192	12.7	1271	4	US-09-949-016-931	Sequence 931, App
32	190	12.6	1104	3	US-09-111-470-1	Sequence 1, Appli
33	189.5	12.6	1104	4	US-09-862-802A-1	Sequence 27, Appli
34	189.5	12.6	712	4	US-09-898-554-27	Sequence 27, Appli
35	183.5	12.2	1348	4	US-09-949-016-4090	Sequence 4090, Ap
36	183.5	12.2	1372	4	US-09-949-016-4432	Sequence 4432, Ap
37	183.5	12.2	1372	4	US-09-949-016-4433	Sequence 4433, Ap
38	183	12.1	402	3	US-08-543-246B-10	Sequence 10, Appli
39	183	12.1	648	3	US-08-543-246B-14	Sequence 14, Appli
40	183	12.1	1755	3	US-08-543-246B-8	Sequence 8, Appli
41	180.5	12.0	378	3	US-08-772-440-9	Sequence 9, Appli
42	180.5	12.0	528	3	US-08-772-440-7	Sequence 7, Appli
43	172.5	11.4	1279	4	US-09-949-016-4430	Sequence 4430, Ap
44	172.5	11.4	1279	4	US-09-949-016-4431	Sequence 4431, Ap
45	171	11.3	1464	4	US-09-949-016-5720	Sequence 5720, Ap

ALIGNMENTS

RESULT 1
US-09-055-095-2
Sequence 2, Application US/09055095
Patent No. 5945308
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Patterson, Chandra
APPLICANT: Corley, Neil C.
APPLICANT: Sather, Susan
TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/055,095
FILING DATE: Filed Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0500 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555

```

; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1740 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGN0T09
; CLONE: 1355922
US-09-055-095-2

Alignment Scores:
Pred. No.: 1.4e-171 Length: 1740
Score: 1465.00 Matches: 275
Percent Similarity: 94.50% Conservative: 0
Best Local Similarity: 94.50% Mismatches: 2
Query Match: 97.15% Indels: 14
DB: 2 Gaps: 1

US-10-689-742-160 (1-280) x US-09-055-095-2 (1-1740)

Qy 4 LysTyrSerSerThrArgAspMetLeuAspAspGlyAspThrMetSerLeuHis 23
Db 5 AAGTACAGCAGCAGCAGGACATGCTGGATGATGATGGGACACCAACATGAGCCTGCAT 64

Qy 24 SerGlnAlaSerAlaThrArgHisProGluProArgArgThrGluHisArgAlaPro 43
Db 65 TCTCAAGCCTGGCCACAGCTCGGCATCCAGAGCCCGGCACAGACAGGCTCCC 124

Qy 44 SerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuValLeuLeu 63
Db 125 TCTTCAACGTGGCGACAGTGGCCCTGACCCCTGCTGACTTTGCTGTTGCTGCTGATA 184

Qy 64 GlyLeuAlaAlaLeuGlyLeuLeu----- 71
Db 185 GGGCTGGCAGCCCTGGGGCTTTTGTGTAACTGTGCGCTCANNCCCTGGGGGAGGATCCTGG 244

Qy 72 -----PhePheGlnTyrTyrGlnLeuSerSerThrGlyGlnAspThrIleSerGlnMet 89
Db 245 TTCCAAGTTTTTCAGTACTACAGCTCTCCAAATCTGGTCAAGACACCATTTCTCAAATG 304

Qy 90 GluGluArgLeuGlyAsnThrSerGlnGluLeuGlnSerLeuGlnValGlnAsnIleLys 109
Db 305 GAAGAAAGATTAGGAATACGTCCCAAGAGTTGCAATCTCTCAAGTCCAGATATAAAG 364

Qy 110 LeuAlaGlySerLeuGlnHisValAlaGluLysLeuCysArgGluLeuTyrAsnLysAla 129
Db 365 CTTCGAGGAAGTCTGCAGCATGTGGCTGAAAAACTCTGCTGAGCTGTATAACAAAGCT 424

Qy 130 GlyAlaHisArgCysSerProCysThrGluGlnTTrpLysTTrpHisGlyAspAsnCysTyr 149
Db 425 GGAGCACACAGTGCAGCCCTTTGTACAGACAAATGGAAATGGCATGGAGACAAATGGCTAC 484

Qy 150 GlnPheTyrLysAspSerLysSerTrpGluAspCysLysTyrPheCysLeuSerGluAsn 169
Db 485 CAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAATATTTCTGCTCTAGTGAAGAAC 544

Qy 170 SerThrMetLeuLysIleAsnLysGlnGluAspLeuGluPheAlaAlaSerGlnSerTyr 189
Db 545 TCTACCATGCTCAAGATATAACAAACAAGAAGACCTGGAAATTTGGCGCGCTCTCAGAGCTAC 604

Qy 190 SerGluPhePheTyrSerTyrTrpThrGlyLeuLeuArgProAspSerGlyLysAlaTrp 209
Db 605 TCTGAGTTTTTCTACTCTTATTTGGACAGGGCTTTTGGCCCTTGGCAGTGGCAAGCCCTGG 664

Qy 210 LeuTrpMetAspGlyThrProPheThrSerGluLeuPheHisIleIleIleAspValThr 229
Db 665 CTGTGGATGGATGGAACCCCTTCTCACTTCTGAACCTGTTCCATATATATATAGATGTAC 724

Qy 230 SerProArgSerArgAspCysValAlaIleLeuAsnGlyMetIlePheSerIleAspCys 249
Db 725 AGCCCAAGAAGCAGAGACTGTGTGGCCATCCTTAATGGGATGATCTTCTCAAGGACTGC 784

Qy 250 LysGluLeuLysArgCysValCysGluArgArgAlaGlyMetValLysProGluSerLeu 269
Db 785 AAAGAAATTGAAGCGTTGTGTCTGTGAGAGAAGGCGAGGAATGGTGAAGCCAGAGCCTC 844

Qy 270 HisValProGluThrLeuGlyGluGlyAsp 280
Db 845 CATGTCCCCCTGAAACATTAGGCGAAGGTGAC 877

RESULT 2
US-09-247-155-52
; Sequence 52, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 52
; LENGTH: 821
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..732
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 46..186
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 9.4
; OTHER INFORMATION: seq LILLILCVGMVVG/LV
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 781..786
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 806..821
US-09-247-155-52

Alignment Scores:
Pred. No.: 1.77e-34 Length: 821
Score: 358.00 Matches: 80
Percent Similarity: 49.63% Conservative: 54
Best Local Similarity: 29.63% Mismatches: 92
Query Match: 23.74% Indels: 44
DB: 3 Gaps: 7

US-10-689-742-160 (1-280) x US-09-247-155-52 (1-821)

Qy 7 SerThrArgAsp---MetLeuAspAspGlyAspThrThrMetSerLeuHisSerGln 25
Db 31 AGTACTCGGAGGCAATGCGAGATGAAGATGATACATCACCTTAATATATTAATAACTCGG 90

Qy 26 AlaSerAlaThrThrArgHisProGluProArgThrGluHisArgAlaProSerSer 45
Db 91 AAACAGCTCTCTGC-----TCGGTTGGCCCTGCATCTCTCTTC 129

Qy 46 ThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuValLeuLeuLeuLeu 65
Db 130 TGGTGGCGTGTGATGGCTTTGATTTCTGCTGATCTGCTGCGTGGGATGGTTGTGCGGCTG 189
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QY 66 AlaAlaLeuGlyLeuLeuPhePheGlnTyrGlnLeuSerAsnThrGlyGlnAspThr 85
Db 190 GTGGCTCTGGGATTTGG----- 207
QY 86 IleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeuSerLeuGlnVal 105
Db 208 ---TCTGTCATGAGCGCAATTAC-----CTACAGAT 237
QY 106 GlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLysLeuCysArg----- 123
Db 238 GAGAAATGAAATCGCACAGCACTCTGCAACAATTAGCAAGCGCTTCTGTCATATG 297
QY 124 -----GluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGlu 139
Db 298 GTAAACAATCAAGCACTTCAAGGCTCAATAAATGCAAGCCCTGTGACACA 357
QY 140 GlnTyrLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGlu 159
Db 358 AACTGGAGATATTATGGAGATAGCTGCTATGGTTCTTCAGGCACAACTTAACATGGAA 417
QY 160 AspCysLysTyrPheCysLeuSerGluAsnSerThrMetLysLysIleAsnLysGlnGlu 179
Db 418 GAGAGTAAGCAGTACTGACATGATGCTACTCTCTGAAGATTGACAACCGGAAC 477
QY 180 AspLeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGly 199
Db 478 ATTGTGGAGTACATCAAGCCAGGACTCAT-----TTAATTCGTTGGGTCGGA 525
QY 200 LeuLeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSer 219
Db 526 TTATCTGCCAGAGTCGAATGAGTCTGGAAGTGGGAGGAGCTCGGTATATCTCAGAA 585
QY 220 GluLeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAlaIle 239
Db 586 AATATGTTTGGATTTTGGAGAT-----GGAAAGGAAATATGATTTGCTTATTTT 639
QY 240 LeuAsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArg 259
Db 640 CATATGGGAAATGCAACCTCTCTGTGGAACAACATATTATTATTTATGTTGAGAGG 699
QY 260 ArgAlaGlyMetValLysProGluSerLeu 269
Db 700 AGGCTGGCATGACCAAGGTGGACCACTA 729

RESULT 3

US-08-690-095-2

Sequence 2, Application US/08690095

Patent No. 5792648

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Au-Young, Janice

APPLICANT: Goli, Surya K.

TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/690,095

FILING DATE: Filed Herewith

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0110 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 970 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

LIBRARY: MFGNOT03

CLONE: 513418

US-08-690-095-2

Alignment Scores:

Pred. No.: 4,766-34 Length: 970

Score: 355.50 Matches: 87

Percent Similarity: 49.80% Conservative: 36

Best Local Similarity: 35.22% Mismatches: 77

Query Match: 23.57% Indels: 47

DB: 1 Gaps: 9

US-10-689-742-160 (1-280) x US-08-690-095-2 (1-970)

QY 42 AlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuValLeu 61
Db 240 GCTCCCTCTCATGTATGGCTCCAGCAGCTTTGTTCTGACTCTTCTGTGCTTCTGTG 299
QY 62 LeuIleGlyLeuAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsnThr 81
Db 300 CTCATTGGATGGGAGTCTTGGCAAGCATGTTTCACTTGAAGATAGAA----- 353
QY 82 GlyGlnAspThrIleSerGlnMetGluArgLeuGlyAsnThrSerGlnGluLeuGln 101
Db 354 -----ATGAAAAAATGAACAACATCAAAACATCAGTGAAGAGCTCCAG 398
QY 102 -----SerLeuGlnVal-----GlnAsnIle-----LysLeu 110
Db 399 AGAAATATTTCTCTACAACTGATGATAGTAACATATATCTCCAACAAGATCAGGAACCTC 458
QY 111 AlaGlySerLeuGlnHisValAlaGluLysLeuCysArgGluLeuTyrAsnLysAlaGly 130
Db 459 TCCACCACACTGCAAAACAATAGCCACCAAAATATGCTGTGAGCTATATAGCAAGAACAA 518
QY 131 AlaHisArgCysSerProCysThrGluGlnTrpLysTrpHisGlyAspAsnCysTyrGln 150
Db 519 GAGCAACAATGTAGCCCTTGTCCAAGGAGATGGATTGGCATAGGACAGACTGTTATTTC 578
QY 151 PheTyrLysAspSerLysSerTrpGluAspCysLysTyrPheCysLeuSerGluAsnSer 170
Db 579 CTAAGTGATGATGTCCAAACATGGCAGGAGAGTAATAATGGCTGTGCTCAGAAATGCC 638
QY 171 ThrMetLeuLysIleAsnLysGlnGluAspLeuPheAlaSerGlnSerTyrSer 190
Db 639 AGCCTGTTGAAGATAAACAACAAATATGCAATTTATATAAATCCAGAGTAGATCA 698
QY 191 GluPhePheTyrSerTyrTrpThrGlyLeu-----Leu 201
Db 699 -----TATGACTATTGGCTGGGATTATCTCTCGAAGAAGATTCACCTCGTGGTAG 749
QY 202 ArgProAsp-----SerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThr 218
Db 750 AGAGTGGATATATATACTCACTCTCTGCTGGGTT---ATAAGAAACGACCTGACITTA 806
QY 219 SerGluLeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAla 238
Db 807 AATACATGTTAT-----TGTGGATAT 827
QY 239 IleLeuAsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGlu 258
Db 828 ATAAATAGACTATATGTTTCAATATTATCACTGCACCTTATAAAAAAAGAAATGATATGTGAG 887

REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 800:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: MPMGN0T03
CLONE: 513418
US-09-016-434-800

Alignment Scores:
Pred. No.: 4,76e-34 Length: 970
Score: 355.50 Matches: 87
Percent Similarity: 49.80% Conservative: 36
Best Local Similarity: 35.22% Mismatches: 77
Query Match: 23.57% Indels: 47
DB: 4 Gaps: 9

US-10-689-742-160 (1-280) x US-09-016-434-800 (1-970)

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QY 42 AlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuLeuThrLeuValLeu 61
Db 240 GCTCCCTCTCATGTATGGCGTCCAGCAGCCTTGTTCGACTCTTCTGTGCCTTCTGTG 299
QY 62 LeuLeuGlyLeuAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsnThr 81
Db 300 CTCATTGGATGGAGCTGTGGCAGCATGTTTCATGTAACTTTGAAGATAGAA----- 353
QY 82 GlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeuGln 101
Db 354 -----ATGAAAAAATGAACAACACTACAAAAACATCATGTGAAGAGCTCCAG 398
QY 102 -----SerLeuGlnVal-----GlnAsnIle-----LysLeu 110
Db 399 AGAAATATTCTCTACAACTGATGAGTAACATGAATATCTCCAACAGATCAGGAACCTC 458
QY 111 AlaGlySerLeuGlnHisValAlaGluLeuLeuCysArgGluLeuTyrAsnLysAlaGly 130
Db 459 TCCACACACTGCACAAATACGACCAAAATATATCGTGAGCTATATAGCAAGAACAA 518
QY 131 AlaHisArgCysSerProCysThrGluGlnTyrLysTrpHisGlyAspAsnCysTyrGln 150
Db 519 GAGCACAATGTAAAGCTTGTCCAGGAGATGGATTGGCATAGGACAGCTGTATTTC 578
QY 151 PheTyrLysAspSerLysSerTrpGluAspCysLysTyrPheCysLeuSerGluAsnSer 170
Db 579 CTAAGTGATGATGTCACAAATGTCAGGAGAGTAAATGGCCTGTGCTCAGAAATGCC 638
QY 171 ThrMetLeuLysIleAsnLysGlnGluAspLeuPheAlaAlaSerGlnSerTyrSer 190
Db 639 AGCGTGTGAAGATAAACAACAAATATGCAATTTTAAATATCCAGAGTAGATCA 698
QY 191 GluPhePheTyrSerTyrTrpThrGlyLeu-----Leu 201
Db 699 -----TATGACTATTGGCTGGGATTTATCTCTGAGAGAGATTCCTCGTGATG 749
QY 202 ArgProAsp-----SerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThr 218
Db 750 AGAGTGGAATAATAATCAACTCTCTGCTGGGTT---ATAAGAAACGACCTGACTTA 806
QY 219 SerGluLeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValala 238
Db 807 AATAACATGTAT-----TGCGATAT 827
QY 239 IleLeuAsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGlu 258
Db 828 ATAATAGACTATATGTTCAATATTATCTGCACTTATATAAAAAAAGAAATGATATGTGAG 887
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QY 259 ArgArgAlaGlyMetValLys 265
Db 888 AGATGGCCAATCCAGTGCAG 908
RESULT 6
US-09-482-273-34
Sequence 34, Application US/09482273
Patent No. 6534631
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PZ030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 1737
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (1674)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (1731)
OTHER INFORMATION: n equals a,t,g, or c
US-09-482-273-34

Alignment Scores:
Pred. No.: 3.87e-33 Length: 1737
Score: 351.50 Matches: 86
Percent Similarity: 49.80% Conservative: 37
Best Local Similarity: 34.82% Mismatches: 77
Query Match: 23.31% Indels: 47
DB: 4 Gaps: 9

US-10-689-742-160 (1-280) x US-09-482-273-34 (1-1737)

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QY 42 AlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuLeuThrLeuValLeu 61
Db 292 GCTCCCTCTCATGTATGGCGTCCAGCAGCCTTGTTCGACTCTTCTGTGCCTTCTGTG 351
QY 62 LeuLeuGlyLeuAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsnThr 81
Db 352 CTCATTGGATGGAGCTTGTGCAAGCATGTTTCATGTAACTTTGAAGATAGAA----- 405
QY 82 GlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeuGln 101
Db 406 -----ATGAAAAAATGAACAACACTACAAAAACATCATGTGAAGAGCTCCAG 450
QY 102 -----SerLeuGlnVal-----GlnAsnIle-----LysLeu 110
Db 451 AGAAATATTCTCTACAACTGATGAGTAACATGAATATCTCCAACAGATCAGGAACCTC 510
QY 111 AlaGlySerLeuGlnHisValAlaGluLeuLeuCysArgGluLeuTyrAsnLysAlaGly 130
Db 511 TCCACACACTGCACAAACAAATATATGCTGAGCTATATAGCAAGAACAA 570
QY 131 AlaHisArgCysSerProCysThrGluGlnTyrLysTrpHisGlyAspAsnCysTyrGln 150
Db 571 GAGCACAATGTAAAGCTTGTCCAAGGAGATGGATTGGCATAGGACAGCTGTATTTC 630
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QY 151 PhetyrLysAspSerLysSerTrpGluAspCysLysTyrPheCysLeuSerGluAsnSer 170
Db 631 CTAAGTGATGATGTCACCAACATGGCAGGAGTAAATGGCTGTGCTGCTCAGAAATGCC 690
QY 171 ThrMetLeuLysIleAsnLysGlnGluAspLeuPheAlaAAsrGlnSerTyrSer 190
Db 691 AGCCTGTTGAAGATAAACAACAATAATGCATTGGAAATTTATAAAATCCAGAGTAGATCA 750
QY 191 GluPhePheTyrSerTyrTrpThrGlyLeu-----Leu 201
Db 751 -----TATGACTATTGGCTGGATATATCTCTGAAGAAGATTCACCTGGGTATG 801
QY 202 ArgProAsp-----SerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThr 218
Db 802 AGAGTGGATAATATAATCAATCTCTGCTGGGT-----ATAAGAAACGCACCTGACTTA 858
QY 219 SerGluLeuPheHisIleIleAspValThrSerProArgSerArgAspCysValAla 238
Db 859 AATAACATGTAT-----TGTTGATAT 879
QY 239 IleLeuAsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGlu 258
Db 880 ATAATAGACTATATGTTCAATATATCACTGCACCTTATAACAAGAAATGATATGTGAG 939
QY 259 ArgArgAlaGlyMetValLys 265
Db 940 AAGATGGCCATCCAGTGCAG 960

RESULT 7

US-08-809-494A-1
; Sequence 1, Application US/08809494A
; Patent No. 5962260
; GENERAL INFORMATION:
; APPLICANT: Sawamura, Tatsuya
; APPLICANT: Masaki, Tomoo
; TITLE OF INVENTION: Modified Low-Density Lipoprotein
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAulay Fisher Nissen Goldberg & Kiel
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,494A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-321705
; FILING DATE: 30-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-214206
; FILING DATE: 31-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; REGISTRATION NUMBER: 24408
; REFERENCE/DOCKET NUMBER: JG-YY-4363PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 986-4090
; TELEFAX: 212 818-9479
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1897 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bos taurus
; TISSUE TYPE: Vascular endothelial cells
; IMMEDIATE SOURCE:
; LIBRARY: Bovine aortic endothelial cell cDNA
; CLONE: pBLOX-1
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 1880..1897
; FEATURE:
; NAME/KEY: misc RNA
; LOCATION: 1859..1864
; OTHER INFORMATION: /function= "PolyA Signal"
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..34
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 848..1897
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 35..847
US-08-809-494A-1

Alignment Scores: 9.92e-28 Length: 1897
Pred. No.: 308.50 Matches: 80
Score: 47.08% Conservative: 41
Percent Similarity: 31.13% Mismatches: 111
Best Local Similarity: 20.46% Indels: 25
Query Match: 2 Gaps: 7
DB:

US-10-689-742-160 (1-280) x US-08-809-494A-1 (1-1897)

QY 33 ProGluProArgArgThrGluHisArgAlaProSerSerThrTrpArgProValAlaLeu 52
Db 83 CCAATGGCAAGACAGCAAAAGTTTGTTCCTCTTGGAGGTGGTACCTGCTGCTGTG 142
QY 53 ThrLeuLeuThrLeuCysLeuValLeuLeuIleGlyLeuAlaLeuGlyLeuPhe 72
Db 143 ACTCTAGGGGTCCTTGTCTGGGATTACTGTGTGCTGTATATATTGTGATACTCAATTA 202
QY 73 PheGlnTyrTyrGlnLeuSerAsnThrGlyGlnAspThrIleSerGlnMetGluGlu 91
Db 203 TCCAGGTCTCTGTATCTCATAAAGAAACAGCAACAATATTACTCCAGGAAGATATC 262
QY 92 -----ArgLeuGlyAsnThrSerGlnGlnLeuSer 102
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Db 323 GAACCTCAAAGAAATGATAGAAACCTTTGCCACAAGCTGGATGAGAAATCCAGAAACTA 382
QY 122 CysArgGluLeuTyrAsn-----LysAlaGlyAlaHis 132
Db 383 ---ATGGAACCTTCCCGCCAGAACCTGAATCTCAAGAAGTTCTGAAAGAGCGCAGCAAC 439
QY 133 ArgCysSerProCysThrGluGlnTrpLysTrpHisGlyAspAsnCysTyrGlnPheTyr 152
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QY 153 LysAspSerLysSerTrpGluAspCysLysTyrPheCysLeuSerGluAsnSerThrMet 172
Db 500 TCTGGCTCTTTTAATTGGAAAAAGCCAGGAGAACTGCTTGTCTTTGGATGCCACTTG 559
QY 173 LeuLysIleLeuLysGlnGluAspLeuPheAlaAlaSerGlnSerTyrSerGluPhe 192
Db 560 CTGAAGATTATAGCACAGATGAATGGAATTC---ATCCAGCAAAATGATTGCCAATTC 616

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QY 213 AspGlyThrProPheThrSerGluLeuPheHisIle-----IleIleAspValThrSer 230
Db 677 GATGGTACTCCITGAGCCCACTTGTGTAGAAATTCAGGGAGCTGTTCCCGTATGTAT 736
QY 231 ProArgSerArgAspCysValAlaIleLeuAsnGlyMetIlePheSerLysAspCysLys 250
Db 737 CCT---TCAGGGACCTGTGCATATATCAAGGGGAACCTGTTTCTGCTGAAAACCTGCATT 793
QY 251 GluLeuLysArgCysValCysGluArgAlaGlyMetValLysProGlu 267
Db 794 TTAAGTGCATTTCAGTATATGTCAAAAGAGGCGAATCTATTGAGACACAG 844

RESULT 8

US-09-352-302-1
Sequence 1, Application US/09352302
Patent No. 6197937
GENERAL INFORMATION:
APPLICANT: Sawamura, Tatsuya
APPLICANT: Masaki, Tomoo
TITLE OF INVENTION: Modified Low-Density Lipoprotein
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAulay Fisher Nissen Goldberg & Kiel
STREET: 261 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/352,302
FILING DATE: 12-JUL-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules E
REGISTRATION NUMBER: 24408
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
TELEFAX: 212 818-9479
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1897 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bos taurus
TISSUE TYPE: Vascular endothelial cells
IMMEDIATE SOURCE:
LIBRARY: Bovine aortic endothelial cell cDNA
CLONE: pBLOX-1
FEATURE:
NAME/KEY: polyA site
LOCATION: 1880..1897

FEATURE:
NAME/KEY: misc RNA
LOCATION: 1859..1864
OTHER INFORMATION: /function= "PolyA signal"

FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..34
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 848..1897
FEATURE:
NAME/KEY: CDS
LOCATION: 35..847
US-09-352-302-1

Alignment Scores:

Pred. No.: 9,92e-28 Length: 1897
Score: 308.50 Matches: 80
Percent Similarity: 47.05% Conservative: 41
Best Local Similarity: 31.13% Mismatches: 111
Query Match: 20.46% Indels: 25
DB: 3 Gaps: 7

US-10-689-742-160 (1-280) x US-09-352-302-1 (1-1897)

QY 33 ProGluProArgArgThrGluHisArgAlaProSerSerThrTrpArgProValAlaLeu 52
Db 83 CCAATGCAAGACAGCAAAAGGTTTGTCTCTTGGAGGTGTACCTCTGCTGCTGTG 142
QY 53 ThrLeuLeuThrLeuValLeuLeuLeuGlyLeuAlaLeuLeuLeuPhe 72
Db 143 ACTTAGGGTCTTTGTCTGGGATTACTGGTACTGTATATTGTTGATTACTGCATTA 202
QY 73 PheGlnTyrTyrGlnLeuSerAsnThrGlyGlnAspThrIleSerGlnMetGluGlu 91
Db 203 TCCAGGCTCTGATCTCATAAAGAAACAGCAAGCAATATTACTCACCAGGAGATATC 262
QY 92 -----ArgLeuGlyAsnThrSerGlnLeuGlnSer 102
Db 263 CTGGAGGGACAGATTTTAGCCCGCAGATCAGAAAAATCTGCCAGGAGTCCACAGAAG 322
QY 103 LeuGlnValGlnAsnIleLys---LeuAlaGlySerLeuGlnHisValAlaGlyLysLeu 121
Db 323 GAACTCAAGAAATGATAGAAACCTTGTCCCAAGCTGGATGAGAAATCCAGAAACTA 382
QY 122 CysArgGluLeuTyrAsn-----LysAlaGlyAlaHis 132
Db 383 ---ATGGAACTTCACCGCAGAACCTGAATCTCCAAGAAAGTTCTGAAAGAGGCGCAAC 439
QY 133 ArgCysSerProCysThrGluGlnTrpLysTrpHisGlyAspAsnCysTyrGlnPheTyr 152
Db 440 TATTCAGGTCTCTTGTCCCAAGACTGCTGGCATGAAGAAACTGTTTACCAATTTCC 499
QY 153 LysAspSerLysSerTrpGluAspCysLysTyrPheCysLeuSerGluAsnSerThrMet 172
Db 500 TCTGCTCTTTTATTTGGAAAAAGCCAGGAGAACTGCTGTCTTTTGGATGCCCTGTG 559
QY 173 LeuLysIleAsnLysGlnGluAspLeuGluPheAlaIleAsnSerGlnSerTyrSerGluPhe 192
Db 560 CTGAAGATTATAGCACAGATGAATTC---ATCCAGCAAAATGATTTCCCATTC 616
QY 193 PheTyrSerTyrTrpThrGlyLeuLeuArgProAspSerGlyLysAlaTrpLeuTrpMet 212
Db 617 AGTTTCCCTTCTGGATGGGTTGTCAATGAGAAACCAATTAATCTCGTGGCTTTGGGAA 676
QY 213 AspGlyThrProPheThrSerGluLeuPheHisIle-----IleIleAspValThrSer 230
Db 677 GATGTACTCTTTTACGCCCTTGTGTAGAAATTCAGGGAGCTGTTCCCGTATGTAT 736
QY 231 ProArgSerArgAspCysValAlaIleLeuAsnGlyMetIlePheSerLysAspCysLys 250
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; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: McAulay Fisher Nissen Goldberg & Kiel
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/352,302
; FILING DATE: 12-JUL-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-321705
; FILING DATE: 30-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-214206
; FILING DATE: 31-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; REGISTRATION NUMBER: 24408
; REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 986-4090
; TELEFAX: 212 818-9479
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1906 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bos taurus
; TISSUE TYPE: Vascular endothelial cells
; IMMEDIATE SOURCE:
; LIBRARY: Bovine aortic endothelial cells cDNA
; CLONE: pBLOX-1
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; NAME/KEY: polyA site
; LOCATION: 1889..1906
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; NAME/KEY: misc RNA
; LOCATION: 1864..1873
; OTHER INFORMATION: /function= "PolyA Signal"
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..34
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 857..1906
; FEATURE:
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; LOCATION: 35..856
; US-09-352-302-3
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; Alignment Scores:
; Pred. No.: 16-27 Length: 1906
; Score: 308.50 Matches: 80
; Percent Similarity: 48.58% Conservative: 40
; Best Local Similarity: 32.39% Mismatches: 100
; Query Match: 20.46% Indels: 27
; DB: 3 Gaps: 8
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; US-10-689-742-160 (1-280) x US-09-352-302-3 (1-1906)

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Db 122 TCCTCTTGGAGGTGGTACCTCTGCTGCTGCTAGGGGTCTTTGTCTGGATTACTG 181
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QY 112 GlySerLeuGlnHisValAlaGluLysLeuCysArgGluLeuTyrAsn----- 127
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RESULT 11
US-08-809-494A-5
; Sequence 5, Application US/08809494A
; Patent No. 5962260
; GENERAL INFORMATION:
; APPLICANT: Sawamura, Tatsuya
; APPLICANT: Masaki, Tomoo
; TITLE OF INVENTION: Modified Low-Density Lipoprotein
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAulay Fisher Nissen Goldberg & Kiel
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,494A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-321705
; FILING DATE: 30-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-214206
; FILING DATE: 31-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; REGISTRATION NUMBER: 24408
; REFERENCE/DOCKET NUMBER: JG-YY-4363PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 986-4090
; TELEFAX: 212 818-9479
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1318 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Lung, placenta
; IMMEDIATE SOURCE:
; LIBRARY: Human lung cDNA
; CLONE: lambdaBdahlOX-1
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; NAME/KEY: 5'UTR
; LOCATION: 66..125
; FEATURE:
; NAME/KEY: 3'UTR
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Db 460 AAGCTGAATGAGAAATCCAAAGAGCAAAATGAATCTCACCACCAAGAAATCTGAATCTCAA 519
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; Qy 112 GlySerLeuGlnHisValAlaGluLysLeuCysArgGluLeuTyrAsnLysAlaGlyAla 131
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; Db 520 GAAACACTGAAGAGAGTAGCA----- 540
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; Qy 171 ThrMetLeuLysIleAsnLysGlnGluAspLeuGluPheAlaAlaSerGln---SerTyr 189
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; Db 658 AAGTGTCTGAAAATTAATAGCAGAGTGTCTGGACTTCATCCAGCAAGCAANTTTCCTAT 717
;   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
; Qy 190 SerGluPhePheTyrSerTyrTrpThrGlyLeuLeuArgProAspSerGlyLysAlaTrp 209
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; RESULT 12
; US-09-352-302-5
; Sequence 5, Application US/09352302
; Patent No. 6197937
; GENERAL INFORMATION:
; APPLICANT: Sawamura, Tatsuya
; APPLICANT: Masaki, Tomoo
; TITLE OF INVENTION: Modified Low-Density Lipoprotein
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAnulay Fisher Nissen Goldberg & Kiel
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/352,302
; FILING DATE: 12-JUL-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-321705
; FILING DATE: 30-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-214206
; FILING DATE: 31-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; REGISTRATION NUMBER: 24408
; REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 986-4090
; TELEFAX: 212 818-9479

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Db 92 AAATATCACTCTCATATAGAAATCTGGATGAAGATGATATCAATAGACTTCAGC 151
Qy 24 SerGlnAlaSerAlaThrArgHisProGluProArgArgThrGlu-----HisArg 41
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Qy 42 AlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuValLeu 61
Db 200 GCTCATCTTCACCTTGGAGGCCCATTCAGCTGGGTAGGAATCCTGTCTTGTGTA 259
Qy 62 LeuLeuGlyLeuAlaLeuGlyLeuLeuPheGlnIleThrGlnLeuSerAsnThr 81
Db 260 GTAGTGGTGTCTGAGTCTGGTCCCTAGCATTTTGGCGACAC-----AATCA 310
Qy 82 GlyGlnAspThrIleSerGlnMetCgluGluArgLeuGlyAsnThrSerGlnGluLeu 101
Db 311 GGGAGAAATCCA-----GAGGAGAAA-----GACAACTTCCTA 343
Qy 102 SerLeuGlnValGlnAsnIleLeuAlaGlySerLeuGlnHisValAlaGluLeu 121
Db 344 TCAAGAAATAAGAGAACACACACCCACAGATCA-----TCTTAGATGAGAGGTG 397
Qy 122 CysArgGluLeuTrpAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGlnTrp 141
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Qy 142 LysTrpHisGlyAspAsnCysThrGlnPheTrpLysAspSerLysSerTrpGluAspCys 161
Db 458 ATCATGCGATGGAAGAGCTGTACTATTATAGCTTCTCAGGAATTCCTGTGTAGGAGT 517
Qy 162 LysTrpPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAspLeu 181
Db 518 AAGAGACACTGCTCCACCTAGGTGCTCATCTACTGAGATGAGCAACTCAAGAAATTT 577
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Qy 222 PheHisIleIleAspValThrSerProArgSer-----ArgAspCysValAla 238
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RESULT 14

US-08-966-316-15

; Sequence 15, Application US/08966316

; Patent No. 5932445

; GENERAL INFORMATION:

; APPLICANT: Lal, Preeti

; APPLICANT: Au-Young, Janice

; APPLICANT: Reddy, Roopa

; APPLICANT: Murry, Lynn E.

; APPLICANT: Mathur, Preeti

; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; STREET: Incyte Pharmaceuticals, Inc.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/966,316

; FILING DATE: Herewith

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0424 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 617 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; IMMEDIATE SOURCE:

; LIBRARY: LUNGN0T04

; CLONE: 764465

; US-08-966-316-15

Alignment Scores:

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Percent Similarity:	50.22%	Conservative:	45
Best Local Similarity:	30.40%	Mismatches:	71
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DB:	2	Gaps:	6

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 Db 430 AGAGAGTAAGCAGTACTGCACTGACATGAATGCTACTCTCTCAAGATTGACAAACCGGAA 489
 QY 179 uAspLeuGluPheAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrG1 199
 Db 490 CATTGTGGAGTACAT-CAAGCCAG-----GACTCATTTAATTCGTT-TGGGTGNG 538
 QY 199 yLeuLeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSe 219
 Db 539 ATTATCTCCGACAGAGTCAATGAGCTGGAAGTGGGANGATGGCTCGGGTATCTCAGN 598
 QY 219 rGluLeuPheHisIlelle 225
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RESULT 15

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 ; Sequence 2, Application US/08688342
 ; Patent No. 5871964
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Hillman, Jennifer L.
 ; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: Fast-SEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/688,342
 ; FILING DATE: Filed Herewith
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 990 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; IMMEDIATE SOURCE:
 ; LIBRARY: MMLRIDT01
 ; CLONE: 515847
 US-08-688-342-2

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 Percent Similarity: 37.55% Conservative: 28
 Best Local Similarity: 26.82% Mismatches: 101
 Query Match: 16.64% Indels: 62
 DB: 4 Gaps: 4

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 QY 24 SerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHisArgAlaPro 43
 Db 132 TTCGACTCTCAAGCAATACAGGATAGCTGTGTTTTCAGAAAGGATCGTGTGTGCA 191
 QY 44 SerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuValLeuLeuIle 63
 Db 192 TCTCCTCTCTGGCGCTCATCTGTAATTTTGGAAATCTCTATGCTGTGTAATCTGGTG 251
 QY 64 GlyLeuAlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsnThrGlyGln 83
 Db 252 GTAGCTGTGCTCGGTACCATG----- 275
 QY 84 AspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeuGlnSerLeu 103
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 QY 124 GluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGlnTrpLysTrp 143
 Db 288 -----AGCCCTTGTCTCTCTTAATTTGGATTATA 314
 QY 144 HisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAspCysLysTyr 163
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 QY 164 PheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAspLeuGluPhe 183
 Db 375 CAATGCTGGCAACTGGGCTCTAATCTCTCAAGATAGACAGCTCAATGAATGGGATTT 434
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 QY 204 AspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGluLeuPheHis 223
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 QY 224 IleIleIleAspValThrSerProArg---SerArgAspCysValAlaIleLeuAsnGly 242
 Db 555 ATCAGAACCCACAGCTACCCCAAGAAACCCATCTCCAATTTGTGTATGGATTACCGTGCA 614
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 Db 675 ATG 677

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	1508	100.0	1841	9 US-09-989-722-318	Sequence 318, App
3	1508	100.0	1841	9 US-09-989-723-318	Sequence 318, App
4	1508	100.0	1841	9 US-09-989-723-318	Sequence 318, App
5	1508	100.0	1841	9 US-09-989-727-318	Sequence 318, App
6	1508	100.0	1841	9 US-09-989-731-318	Sequence 318, App
7	1508	100.0	1841	9 US-09-989-732-318	Sequence 318, App
8	1508	100.0	1841	9 US-09-991-073-318	Sequence 318, App
9	1508	100.0	1841	9 US-09-990-442-318	Sequence 318, App
10	1508	100.0	1841	9 US-09-991-163-318	Sequence 318, App
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26	1508	100.0	1841	10 US-09-990-441-318	Sequence 318, App
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36	1508	100.0	1841	10 US-09-991-157-318	Sequence 318, App
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45	1508	100.0	1841	10 US-09-997-628-318	Sequence 318, App

ALIGNMENTS

RESULT 1
US-09-746-783-159
; Sequence 159, Application US/09746783
; Publication No. US20030044935A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; McCoy, John M.
; LaVallie, Edward R.
; Racie, Lisa A.
; Treacy, Maurice
; Spaulding, Vikki
; Agostino, Michael J.
; Howes, Steven H.
; Rehtel, Kim
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; ENCODING THEM

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Qy	161	CysLysTyrPheCysLeuSerGluAasnSerThrMetLeuLysIleAsnLysGlnGluAsp	180	
Db	549	TGTAATAATTCTCGCCTTAGTGAAAACTCTACCATGCTGAAGATAAAACAACAAGAAC	608	
Qy	181	LeuGluPheAlaIaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu	200	
Db	609	CTGGAATTTGCCCGGCTCTCAGAGCTACTCTCAGTTTTTCTACTCTTATTTGGACAGGGCTT	668	
Qy	201	LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu	220	
Db	669	TTGCGCCTTGACATGGCAGGCCCTGGCTGTGGATGGATGGAAACCCCTTCACTTCTGAA	728	
Qy	221	LeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValaIaIleLeu	240	
Db	729	CTGTTCCATATTATAATAGATGTCACCAGCCCAAGACAGAGACTGTGTGGCCATCCCT	788	
Qy	241	AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg	260	
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RESULT 2
US-09-989-722-318

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US-09-389-722-318
; Sequence 318, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoysers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-689-742-160 (1-280) x US-09-989-722-318 (1-1841)

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Db 204 AGCTGCAATTTCTCAAGCTCTGCCACAACCTGGCATCCAGAGCCCGCGGCACAGAGC 263
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Db 264 AGGGCTCCTCTTCAACGTGGCAGCAGTGGCCCTGACCTGCTGACTTTGTGTGGTG 323
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; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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;; PRIOR FILING DATE: 1998-07-09

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; APPLICANT: Eaton, Dan L.
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 1,18e-178 Length: 1841
Score: 1508.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-689-742-160 (1-280) x US-09-989-279-318 (1-1841)

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Db 204 AGCTGTCATTCTCAAGCCTCTGCCCAACTCGGCATCCAGAGCCCGGGGACACAGAC 263
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Db 264 AGGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCCCTGCTGCTGCTGGTGTG 323
QY 61 LeuLeuIleGlyLeuAlaAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsn 80
Db 324 CTGCTGATAGGCTGGCAGCCCTGGGGCTTTTGTGTTTTTTCAGTACTACAGCTCTCCAAT 383
QY 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
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QY 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120
Db 444 CAATCTCTTCAAGTCCAGATATAAGCTTCAGGAGAGCTTCGCAGCATGTGGCTGAAAAA 503
QY 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGln 140
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Db 804 CTGTTCCATATTATATAGATGTCCAGCCCAAGACAGACAGCTGTGTGGCCATCTCTC 863
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Db 864 AATGGATGATCTTCTCAAGSACTGCAAGAAATTGAAGCGTTGTGTCTGTGAGAGAAGG 923
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US-09-989-727-318
; Sequence 318, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLC65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
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/ PRIOR APPLICATION NUMBER: 60/091982
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09

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RESULT 7
US-09-989-732-318
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Patent No. US20020123463A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zenin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC57
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match: 100.00 Indels: 0
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QY 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
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; Patent No. US2002012756A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C15
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; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
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; APPLICANT: Desnoyers, Luc
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QY 221 LeuPheHisIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu 240
DB 804 CTGTTCATATTAATATAGATGTCAACAGCCCAAGAGCAGAGCTGTGTGGCCATCTCTC 863
QY 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
DB 864 AATGGATGATCTTCTCAAGAGCTGCAAGAAATTAAGCGTGTGTCTGTGAGAGAGG 923
QY 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGlyAsp 280
DB 924 GCAGGAAATGTTGAGCCAGAGAGCTTCAATGTCCCCCTGAAACATTAGGCGAAGGTGAC 983
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RESULT 10

US-09-991-163-318
; Sequence 318, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC17
CURRENT APPLICATION NUMBER: US/09/991,163
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05

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RESULT 11

US-09-993-604-318
; Sequence 318, Application US/09993604
; Patent No. US20020137075A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14

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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	1.18e-178	Length:	1841
Score:	1508.00	Matches:	280
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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US-10-689-742-160 (1-280) x US-09-993-604-318 (1-1841)

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Qy	21	SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis	40
Db	204	AGCCTGCATCTCAAGCCTCTGCCCAACTCGGCATCCAGAGCCCGGGCGCAGAGCAGC	263
Qy	41	ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal	60
Db	264	AGGGCTCCCTCTTCAACGTGGCGACCATGTGGCCCTGACCCCTGCTGATTTTGTGTTGGTG	323
Qy	61	LeuLeuLeuGlyLeuAlaAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsn	80
Db	324	CTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTGTTTTCAGTACTACCACTCTCCAAT	383
Qy	81	ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu	100
Db	384	ACTGGTCAGACACCATTTCTCAATGGAGAAAGATTAGGAATACGTCCCAAGATTG	443
Qy	101	GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys	120
Db	444	CAATCTCTCAAGTCCAGAAATATAAGCTTGACAGAGTCTGCAGCATGTGGCTGAAAAA	503
Qy	121	LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln	140
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Qy	141	TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp	160
Db	564	TGGAAATGGCATGGAGACAAATTGCTACAGTTCTATAAGACACACAAAGTTGGAGGAC	623
Qy	161	CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp	180
Db	624	TGTAATATTTCCTGCCCTTAGTAAAACTCTACCATGTCTGAAGATAAAACAAACAAAGAC	683
Qy	181	LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGluLeu	200
Db	684	CTGGAATTTGCCGCTCTCAGAGCTACTCTGAGTTTTTTTCTACTTATTATGACAGGGCTT	743

QY 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
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744 TTGGCCCTTCAGAGTGGCAGGCTGGCTGTGTGATGGATGGAACTTTCATCTCGAA 803
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QY 241 AenGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArg 260
Db |||||
864 AATGGATGATCTTCTCAAGGACTGCAAGAAATTGAAGCGTGTGTCTGTGAGAGAAG 923
QY 261 AlaGlyMetValLysProGluSerLeuHisValProGluThrIleuGlyGluAsp 280
Db |||||
924 GCAGGAATGGTGAAGCCAGAGAGCTTCATGTCCCCCTGAAACATTAGGCGAAGGTGAC 983

RESULT 12
US-09-990-456-318
; Sequence 318, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC22
; CURRENT APPLICATION NUMBER: US/09/990,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 118e-178 Length: 1841
Score: 1508.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Qy 61 LeuLeuLeuGlyLeuAlaAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsn 80
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444 CAATCTCTCAAGTCCAGAAATATAAGCTTGACAGAGTCTGCAGCATGTGGCTGAAAAA 503
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; Patent No. US20020142961A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C55
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CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Iuc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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 ; PRIOR FILING DATE: 1998-07-09

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 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zenin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C66
 ; CURRENT APPLICATION NUMBER: US/09/989,293A
 ; PRIOR FILING DATE: 2001-11-20
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58	PRIOR APPLICATION NUMBER: 60/089512	
59	PRIOR FILING DATE: 1998-06-16	
60	PRIOR APPLICATION NUMBER: 60/089514	
61	PRIOR FILING DATE: 1998-06-16	
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63	PRIOR FILING DATE: 1998-06-17	
64	PRIOR APPLICATION NUMBER: 60/089538	
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66	PRIOR APPLICATION NUMBER: 60/089598	
67	PRIOR FILING DATE: 1998-06-17	
68	PRIOR APPLICATION NUMBER: 60/089599	
69	PRIOR FILING DATE: 1998-06-17	
70	PRIOR APPLICATION NUMBER: 60/089600	
71	PRIOR FILING DATE: 1998-06-17	
72	PRIOR APPLICATION NUMBER: 60/089653	
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1	PRIOR APPLICATION NUMBER: 60/089801
2	PRIOR FILING DATE: 1998-06-18
3	PRIOR APPLICATION NUMBER: 60/089907
4	PRIOR FILING DATE: 1998-06-18
5	PRIOR APPLICATION NUMBER: 60/089908
6	PRIOR FILING DATE: 1998-06-18
7	PRIOR APPLICATION NUMBER: 60/089947
8	PRIOR FILING DATE: 1998-06-19
9	PRIOR APPLICATION NUMBER: 60/089948
10	PRIOR FILING DATE: 1998-06-19
11	PRIOR APPLICATION NUMBER: 60/089952
12	PRIOR FILING DATE: 1998-06-19
13	PRIOR APPLICATION NUMBER: 60/090246
14	PRIOR FILING DATE: 1998-06-22
15	PRIOR APPLICATION NUMBER: 60/090252
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17	PRIOR APPLICATION NUMBER: 60/090254
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19	PRIOR APPLICATION NUMBER: 60/090349
20	PRIOR FILING DATE: 1998-06-23
21	PRIOR APPLICATION NUMBER: 60/090355
22	PRIOR FILING DATE: 1998-06-23
23	PRIOR APPLICATION NUMBER: 60/090429
24	PRIOR FILING DATE: 1998-06-24
25	PRIOR APPLICATION NUMBER: 60/090431
26	PRIOR FILING DATE: 1998-06-24
27	PRIOR APPLICATION NUMBER: 60/090435
28	PRIOR FILING DATE: 1998-06-24
29	PRIOR APPLICATION NUMBER: 60/090444
30	PRIOR FILING DATE: 1998-06-24
31	PRIOR APPLICATION NUMBER: 60/090445
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39	PRIOR APPLICATION NUMBER: 60/090542
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41	PRIOR APPLICATION NUMBER: 60/090557
42	PRIOR FILING DATE: 1998-06-24
43	PRIOR APPLICATION NUMBER: 60/090676
44	PRIOR FILING DATE: 1998-06-25
45	PRIOR APPLICATION NUMBER: 60/090678
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47	PRIOR APPLICATION NUMBER: 60/090690
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51	PRIOR APPLICATION NUMBER: 60/090862
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55	PRIOR APPLICATION NUMBER: 60/091360
56	PRIOR FILING DATE: 1998-07-01
57	PRIOR APPLICATION NUMBER: 60/091478
58	PRIOR FILING DATE: 1998-07-02
59	PRIOR APPLICATION NUMBER: 60/091544
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61	PRIOR APPLICATION NUMBER: 60/091519
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65	PRIOR APPLICATION NUMBER: 60/091633
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67	PRIOR APPLICATION NUMBER: 60/091978
68	PRIOR FILING DATE: 1998-07-07
69	PRIOR APPLICATION NUMBER: 60/091982
70	PRIOR FILING DATE: 1998-07-07

! PRIOR FILING DATE: 1998-07-07
! PRIOR APPLICATION NUMBER: 60/092182
! PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	1.18e-178	Length:	1841
Score:	1508.00	Matches:	280
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-689-742-160 (1-280) x US-09-989-293A-318 (1-1841)

QY	1	MetGlnAlaLysTyrSerThrArgAspMetLeuAspAspGlyAspThrThrMet	20
DB	144	ATGAGGCCAAGTACAGCAGCAGGAGCATGCTGGATGATGATGGGGACACCACTATG	203
QY	21	SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis	40
DB	204	AGCCTGCATTTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCGGGGCACAGGCAC	263
QY	41	ArgAlaProSerSerThrTyrArgProValAlaLeuThrLeuLeuThrCysLeuVal	60
DB	264	AGGGCTCCCTCTTCAACGTGGCGACCACTGGGCCCTGACCCCTGCTGACTTTGTCTTGGTG	323
QY	61	LeuLeuIleGlyLeuAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsn	80
DB	324	CTGCTGATAGGCTGGCAGCCCTGGGGCTTTTGTGTTTTCAGTACTACAGCTCTCCAAT	383
QY	81	ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyValAsnThrSerGlnGluLeu	100
DB	384	ACTGCTCAAGACACCACTTCTCAATGGAAGAAAGATTAGGAATACGTCCTCCAGAGTTG	443
QY	101	GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys	120
DB	444	CAATCTCTTCAAGTCCAGAAATATAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAA	503
QY	121	LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln	140
DB	504	CTCTGCTGTGAGCTGTATAACAAAGCTGGAGCACAGGTGGAGCCCTGTACAGAAACA	563
QY	141	TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp	160
DB	564	TGGAATGGCATGGAGACAATTTGCTACCACTTCTATTAAGACAGCAAAAGTTGGAGGAC	623
QY	161	CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp	180
DB	624	TGTAATATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAAACAACAAGAGAC	683
QY	181	LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu	200
DB	684	CTGGAAATTTGGCGCTCTCAGAGCTACTCTGAGTITTTTCTACTCTTATTGGACAGGGCTT	743
QY	201	LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu	220
DB	744	TTGGCCCTTGACAGTGGCAAGCCCTGGCTGTGGATGGATGGNACCCCTTTCACTTCTGAA	803
QY	221	LeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu	240
DB	804	CTGTTCCATATTATATAGATGTCAACAGCCCAAGAGCAGAGACTGTGTGGCCATCCTC	863
QY	241	AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg	260
DB	864	AATGGGATGATCTTCTCAAGGACTGCAAGAAATTAAGCGTGTGTCTGTGAGAGAAGG	923
QY	261	AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp	280
DB	924	CGAGGAATGGTAAGCCAGAGAGCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGAC	983

Search completed: October 8, 2005, 04:31:49
Job time : 930.136 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 8, 2005, 00:33:43 ; Search time 4098.18 Seconds
(without alignments)
2600.664 Million cell updates/sec

Title: US-10-689-742-160
Perfect score: 1508
Sequence: 1 MQAKYSTRDMLDDDDTTM.....AGMKPESLHVPPETLSEGD 280

Scoring table: BLOSUM62

-O=/cpn2_1/USPTO spool_p/US10689742/runat_07102005_183118_27976/app_query.fasta_1.718
-DB=EST_QPWT=fastp -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0 -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DPSLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV=xlp

-O=/cpn2_1/USPTO spool_p/US10689742/runat_07102005_183118_27976/app_query.fasta_1.718
-DB=EST_QPWT=fastp -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0 -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10689742 @CNC 1.1.6628 @runat_07102005_183118_27976 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DPSLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

1: gb_est1: *
2: gb_est2: *
3: gb_hcc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1504	99.7	1003	3	CR604680 full-length
2	1504	99.7	1671	3	CR614400 full-length
3	1504	99.7	1692	3	CR591231 full-length
4	1504	99.7	1734	3	CR591145 full-length
5	1492	98.9	1045	5	CR591145 full-length
6	1490	98.8	1673	3	CR606141 full-length
7	1480	98.1	1747	3	CR619172 full-length
8	1458	96.7	1759	3	CR598502 full-length
9	1446.5	95.9	927	5	CR598502 full-length

c	10	1442	95.6	914	5	EX391810
	11	1438.5	95.4	1049	1	AL541315
	12	1431.5	94.9	1001	5	EX324788
	13	1422.5	94.3	958	5	EX399696
	14	1410	93.5	1076	5	EX337172
	15	1393.5	92.4	964	5	EX339075
	16	1390.5	92.2	1042	5	EX380212
	17	1371	90.9	919	5	BQ722745
	18	1297	86.0	770	5	EX380079
	19	1287.5	85.4	1078	5	BM920364
	20	1228	81.4	830	4	BI819167
	21	1146	75.0	801	6	CB993235
	22	1105	73.3	819	6	CB992328
	23	1030.5	68.3	1400	3	AK049608
	24	1025.5	68.0	3084	3	AK031121
	25	1019	67.6	832	6	CB996109
	26	973.5	64.6	927	5	BP433855
	27	914	60.6	574	5	BP367597
	28	908	60.2	4988	3	AK036846
	29	907.5	60.2	821	6	CB997137
	30	899	59.6	582	5	BP321061
	31	884	58.6	581	5	BP308484
	32	868	57.6	732	5	EX106079
	33	809	53.6	690	5	EX358767
	34	797	52.9	614	6	CB990793
	35	782.5	51.9	651	2	BB652586
	36	755	50.1	489	7	CV030254
	37	724.5	48.0	901	6	CB991060
	38	686.5	45.5	657	2	BB636547
	39	676.5	44.9	649	7	CF913792
	40	661.5	43.9	648	6	BY734088
	41	656.5	43.5	639	2	BB620369
c	42	652	43.2	373	4	BF988093
	43	645	42.8	774	6	CB554225
	44	642.5	42.6	589	6	CB453572
	45	629	41.7	405	7	R91686

ALIGNMENTS

CR604680 1003 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0D1081YG24 of Placenta Cot 25-normalized
of Homo sapiens (human).

ACCESSION CR604680
VERSION CR604680.1 GI:50485487
KEYWORDS HTC; CNSLT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1003)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paradise Avenue

REFERENCE 2 (bases 1 to 1003)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES Location/Qualifiers

source

1..1003
/organism="Homo sapiens"

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/mol_type="mrna"
/db_xref="taxon:9606"
/clone="CS0D1036YF24"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Alignment Scores:
Pred. No.:      2,28e-152      Length:      1003
Score:          1504.00        Matches:      279
Percent Similarity: 99.64%      Conservative: 0
Best Local Similarity: 99.64%      Mismatches:  1
Query Match:      99.73%      Indels:      0
DB:              3            Gaps:        0

US-10-689-742-160 (1-280) x CR604680 (1-1003)

Qy 1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMet 20
Db 57 ATGCAGGCCAAGTACAGCAGCAGCAGGAGCATGCTGGATGATGATGGGACACCAACATG 116
Qy 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40
Db 117 AGCCTGCAATTTCTCAGAGCTTGGCCAACTCGGCATCCAGAGCCCGCGGCACAGAGC 176
Qy 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal 60
Db 177 AGGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCTGCTGACATTTGTGCTGTG 236
Qy 61 LeuLeuIleGlyLeuAlaAlaLeuGlyLeuLeuPheGlnTyrGlnLeuSerAsn 80
Db 237 CTGCTGATAGGGCTGGCAGCCCTGGGGCTTTGTTTTTTCAGTACTACAGCTCTCCAAT 296
Qy 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
Db 297 ACTGTCAGACACCATTTCTCAATGGAAGAAAGATTAGAAATACCTCCCAAGAGTTG 356
Qy 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120
Db 357 CAATCTCTTCAAGTCCAGAAATAAAGCTTGCAGGAAGCTTGCAGCATGTGGCTGMAAAA 416
Qy 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
Db 417 CTCGTGCTGAGCTGTATACAAAGCTGGACACACAGGTGCAGCCCTTGTACAGAACAA 476
Qy 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
Db 477 TGGAAATGGCATGGAGCAATTTGCTACAGTTCTATAAAGACAGCAAAAGTTGGAGGAC 536
Qy 161 CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
Db 537 TGTAATAATTTCTGCCTTAGTGAATACTCTACCATGCTGAAGATAAACAACAAGAGAC 596
Qy 181 LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu 200
Db 597 CTGGAATTTGGCGGTCTCAGAGCTACTCTCAGATTTTCTACTCTCTATTGACAGGGCTT 656
Qy 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
Db 657 TTGGCCCTGACAGTGGCAAGCCTGGCTGGATGGATGGAAACCCCTTTCACCTCTGAA 716
Qy 221 LeuPheHisIleIleAlaAspValThrSerProArgSerArgAspCysValAlaIleLeu 240
Db 717 CTGTTCCATATTATAATAGATGTCAACAGGCCAAGACAGAGACTGTGTGGCCATCCTT 776
Qy 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
Db 777 AATGGATGATCTTCTCTCAAGGACTGCAAGAAATTGAAGCGTTGTGTCTGTCAGAGAGG 836
Qy 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280
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RESULT 2

CR614400

LOCUS

DEFINITION

CR614400 1671 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0D1036YF20 of Placenta Cot 25-normalized
of Homo sapiens (human).

ACCESSION

CR614400

VERSION

CR614400.1 GI:50495207

KEYWORDS

HTC; CNSLT cDNA.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1671)

AUTHORS

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished

REMARK

Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue
Redwood City, CA 94061
2 (bases 1 to 1671)

REFERENCE

2 (bases 1 to 1671)

AUTHORS

Genoscope.

TITLE

Direct Submission

JOURNAL

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT

- Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES

Location/Qualifiers

1..1671

/organism="Homo sapiens"

/mol_type="mrna"

/db_xref="taxon:9606"

/clone="CS0D1036YF20"

/tissue_type="Placenta Cot 25-normalized"

/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:

Pred. No.: 4.88e-152 Length: 1671

Score: 1504.00 Matches: 279

Percent Similarity: 99.64% Conservative: 0

Best Local Similarity: 99.64% Mismatches: 1

Query Match: 99.73% Indels: 0

DB: 3 Gaps: 0

US-10-689-742-160 (1-280) x CR614400 (1-1671)

Qy 1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMet 20

Db 10 ATGCAGGCCAAGTACAGCAGCAGCAGGAGCATGCTGGATGATGATGGGACACCAACATG 69

Qy 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40

Db 70 AGCCTGCAATTTCTCAGAGCTTGGCCAACTCGGCATCCAGAGCCCGCGGCACAGAGC 129

Qy 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal 60

Db 130 AGGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCTGCTGCTGTGTGTG 189

Qy 61 LeuLeuIleGlyLeuAlaAlaLeuGlyLeuLeuPheGlnTyrGlnLeuSerAsn 80

Db 190 CTGCTGATAGGGCTGGCAGCCCTGGGGCTTTGTTTTTTCAGTACTACAGCTCTCCAAT 249

Qy 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100

Db 250 ACTGGTCAAGACACCATTTCTCAAAATGGAAGAAATAGGAATAGCTCCCAAGAGTTG 309

Qy 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120

Db 310 CAATCTCTTCAAGTCCAGAAATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAA 369

QY 121 LeuCyAsArgGluLeuTyAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
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 Db 370 CTCTGCTGAGCTGTATACAAAGCTGGAGCACACAGGTGCGAGCCCTTGTACAGAAACA 429
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 QY 141 TrpLysTrpHisGlyAspAsnCyStyTrpGlnPheTyLysAspSerLysSerTrpGluAsp 160
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 Db 430 TGGAAATGGCATGGAGACAAATGCTACAGTCTATTAAGACAGACAAAGTTGGGAGAC 489
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 QY 161 CysLysTrpPheCysLeuSerGluAsnSerThrMetLeuLysLeuLysLeuLysLeuLys 180
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 Db 490 TGTAAATATTTCTGCTTAGTGAAACCTCTACCATGCTGAAGATAAACAAACAGAGAC 549
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 QY 181 LeuGluPheAlaAlaSerGlnSerTySerGluPhePheTySerTyTrpThrGlyLeu 200
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 Db 550 CTGGAATTTGGCGCGTCTCAGAGCTACTCTGAGTTTCTTACTCTTATTGGACAGGGCTT 609
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 QY 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
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 Db 610 TTGCCCTCTGACAGTGGCAGGCCCTGGCTGTGGATGGATGGNACCCCTTCTCTGAA 669
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 QY 221 LeuPheHisIleIleAlaSerValThrSerProArgSerArgAspCysValAlaIleLeu 240
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 Db 670 CTGTTTCCATATTTAATAGATGTACACAGCCCAAGAGAGAGAGCTGTGTGGCCATCCTT 729
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 QY 241 AsnGlyMetIlePheSerLysAspCysLysGluLysLysLysLysLysLysLysLys 260
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 Db 730 AATGGGATGATCTTCTCAAGAGACTGCAAGAAATTTGAAGCGTTGTCTGTGAGAGAGG 789
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 Db 790 GCAGGAATGGTGAAGCCAGAGAGCCTCCATGTGCCCCCTGAAACATTAGGCGAAGTGAC 849
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RESULT 3

CR591231 1692 bp mRNA linear HTC 21-JUL-2004
 full-length cDNA clone CS0D1041YA14 of Placenta Cot 25-normalized
 of Homo sapiens (human).

ACCESSION

CR591231

VERSION

CR591231.1 GI:50472038

KEYWORDS

HTC; CNSLT cDNA.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

AUTHORS

Full-length cDNA libraries and normalization

JOURNAL

Unpublished

REMARK

Contact : Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue
 Genoscope.
 2 (bases 1 to 1692)

REFERENCE

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.

FEATURES

Location/Qualifiers

source

1..1692

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0D1041YA14"

/tissue_type="Placenta Cot 25-normalized"

/plasmid="pCMVSPORT_6"

ORIGIN

CR591145 full-length cDNA clone CS0D1049YB09 of Placenta Cot 25-normalized
 of Homo sapiens (human).
 CR591145
 CR591145.1 GI:50471952

Alignment Scores:

Pred. No.: 4,97e-152 Length: 1692

Score: 1504.00 Matches: 279

Percent Similarity: 99.64% Conservative: 0

Best Local Similarity: 99.64% Mismatches: 1

Query Match: 99.73% Indels: 0

DB: 3 Gaps: 0

US-10-689-742-160 (1-280) x CR591231 (1-1692)

QY 1 MetGlnAlaLysTySerSerThrArgAspMetLeuAspAspGlyAspThrThrMet 20
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 Db 45 ATGCAGGCCAAGTACAGCAGCAGCAGGACATGCTGGATGATGATGGGACACACCACCATG 104
 |||||
 QY 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40
 |||||
 Db 105 AGCCTGCATTCTCAAGGCTCTGCCCAACTCGGCATCCAGAGCCCGCGCAGACAGAC 164
 |||||
 QY 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuVal 60
 |||||
 Db 165 AGGGCTCCCTCTTCAACGTGGCAGCAGTGGCCCTGACCCCTGCTGCTGCTTGTGCTGTG 224
 |||||
 QY 61 LeuLeuIleGlyLeuAlaAlaLeuGlyLeuLeuPhePheGlnTyTrpGlnLeuSerAsn 80
 |||||
 Db 225 CTGCTGATAGGCTGGCAGCCCTGGGGCTTTTGTGTTTTCAGTACTACCAGCTCTCCAAT 284
 |||||
 QY 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
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 Db 285 ACTGCTCAAGACACCATTTCTCAATGAAGAAAGATTAGGAAATACGTCCTCCAGAGTTG 344
 |||||
 QY 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120
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 Db 345 CAATCTCTTCAAGTCCAGAAATATAAGCTTGCAGGAAGTCTGCAGCATGTGCTGAAATA 404
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 QY 121 LeuCyAsArgGluLeuTyAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
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 Db 405 CTCTGCTGAGCTGTATACAAAGCTGGAGCACACAGGTGCGAGCCCTTGTACAGAAACA 464
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 QY 141 TrpLysTrpHisGlyAspAsnCyStyTrpGlnPheTyLysAspSerLysSerTrpGluAsp 160
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 Db 465 TGGAAATGGCATGGAGACAAATTGTCTACAGTCTTATTAAGACAGACAAAGTTGGGAGAC 524
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 QY 161 CysLysTrpPheCysLeuSerGluAsnSerThrMetLeuLysLeuLysLeuLysLeuLys 180
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 Db 525 TGTAAATATTTCTGCTTAGTGAAACCTCTACCATGCTGAAGATAAACAAACAGAGAC 584
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 QY 181 LeuGluPheAlaAlaSerGlnSerTySerGluPhePheTySerTyTrpThrGlyLeu 200
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 Db 585 CTGGAATTTGGCGCGTCTCAGAGCTACTCTGAGTTTCTTACTCTTATTGGACAGGGCTT 644
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 QY 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
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 Db 645 TTGGCCCTGACAGTGGCAGGCCCTGGCTGTGGATGGATGGAAACCCCTTTCATCTCTGAA 704
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 Db 705 CTGTTCCATATTTAATAGATGTACAGGCCCAAGAGAGAGACTGTGTGGCCATCCTT 764
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 QY 241 AsnGlyMetIlePheSerLysAspCysLysGluLysLysLysLysLysLysLysLys 260
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 Db 765 AATGGATGATCTTCTCAAGAGACTGCAAGAAATTTGAAGCGTTGTCTGTGAGAGAGG 824
 |||||
 QY 261 AlaGlyMetValLysProGluSerLeuHisValProGluThrLeuGlyGluGlyAsp 280
 |||||
 Db 825 GCAGGAATGGTGAAGCCAGAGAGCCTCCATGTGCCCCCTGAAACATTAGGCGAAGTGAC 884
 |||||

RESULT 4

CR591145

LOCUS

full-length cDNA clone CS0D1049YB09 of Placenta Cot 25-normalized

DEFINITION

of Homo sapiens (human).

ACCESSION

CR591145

VERSION

CR591145.1 GI:50471952

KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1734)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Peng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
REFERENCE 2 (bases 1 to 1734)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES Location/Qualifiers
 source
 1..1734
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS001041YB09"
 /tissue_type="Placenta Cot 25-normalized"
 /plasmid="pCMVSPORT_6"
ORIGIN
 Alignment Scores:
 Pred. No.: 5.16e-152 Length: 1734
 Score: 1504.00 Matches: 279
 Percent Similarity: 99.64% Conservative: 0
 Best Local Similarity: 99.64% Mismatches: 1
 Query Match: 99.73% Indels: 0
 DB: 3 Gaps: 0
 US-10-689-742-160 (1-280) x CR591145 (1-1734)
 Qy 1 MetGlnAlaLysTyrSerThrArgAspMetLeuAspAspGlyAspThrMet 20
 Db 45 ATGAGGCCAAGTACAGCAGCAGGAGCATGTGGATGATGGGACACCACTG 104
 Qy 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40
 Db 105 AGCCTGCATTCTCAAGGCTCTGCCAACACTCGGCATCCAGAGCCCGCGCACAGAGCAC 164
 Qy 41 ArgAlaProSerSerThrTrrArgProValAlaLeuThrLeuLeuLeuVal 60
 Db 165 AGGGCTCCCTCTTCAACGTGGCGACCAAGTGGCCCTGACCTTGTGCTGGTG 224
 Qy 61 LeuLeuLeGlyLeuAlaAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsn 80
 Db 225 CTGCTGATAGGCTGGCAGCCCTGGGGCTTTGTTTTTTCAGTACTACCACTCTCCAT 284
 Qy 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
 Db 285 ACTGGTCAAGACACCATTTCTCAATGAAGAAAGATTAGGAATAGCTCCCAAGAGTTG 344
 Qy 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120
 Db 345 CAATCTCTTCAAGTCCAGATATAAGCTTCAGAGAAAGTCTGCAGCATGTGGCTGAAAAA 404
 Qy 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
 Db 405 CTCTGTGCTGAGCTGTATAAAGAGCTGGACACACAGGTGACGCCCTTGTACAGAACAA 464
 Qy 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160

465 TGGAAATGGCATGGAGACAAATTGCTACCAAGTTCTATAAAGACAGCAAAAGTTGGGAGGAC 524
 Qy 161 CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
 Db 525 TGTAAATATTCTGCTTGTAGTAAACTCTACCACTGTGTAAGATAAACAAGAGAC 584
 Qy 181 LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu 200
 Db 585 CTGGAATTTGCGGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTTAGACAGGGTT 644
 Qy 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
 Db 645 TTGGCCCTGACAGTGGCAAGGCTGGCTGGATGGATGGAAGAACCCCTTTTCACTTCTCAA 704
 Qy 221 LeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu 240
 Db 705 CTGTTCCATATTATATAGATGTCCAGAGCCCAAGAGACAGAGACTGTGTGCGCCATCCTT 764
 Qy 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
 Db 765 AATGGATGATCTTCTCAAGGACTGCAAGAAATGAAGCGTTGTGTCTGTGAGAGAGG 824
 Qy 261 AlaGlyMetValLysProGluSerLeuHisValProGluThrLeuGlyGluGlyAsp 280
 Db 825 GCAGGAATGGTGAAGCCAGAGAGGCTCCATGTGCCCCCTGAAACATTAGGCGAAGGTGAC 884
RESULT 5
 BX379905 1045 bp mRNA linear EST 23-APR-2004
LOCUS BX379905 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS01041YA14 5-PRIME, mRNA sequence.
ACCESSION BX379905
VERSION BX379905.2 GI:46557568
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1045)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 8, 2003 this sequence version replaced gi:30439428.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6541.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS01041BA07QPl&c=6541.r.
FEATURES Location/Qualifiers
 source
 1..1045
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS01041YA14"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Alignment Scores:
 Pred. No.: 4.89e-151 Length: 1045
 Score: 1492.00 Matches: 277
 Percent Similarity: 98.93% Conservative: 0

Best Local Similarity: 98.93% Mismatches: 3
 Query Match: 98.94% Indels: 0
 DB: 5 Gaps: 0

US-10-689-742-160 (1-280) x BX379905 (1-1045)

QY 1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMet 20
 DB 45 ATGAGGCCAAGTACAGACGACGAGGACATGCTGGATGATGATGGGACACCAATG 104

QY 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProProArgThrGluHis 40
 DB 105 AGCTTGCATTTCTCAAGGCTCTGCCAACACTCGGATCCAGACCCCGGGGACAGAGAC 164

QY 41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal 60
 DB 165 AGGGCTCCCTCTTCAAGCTGGGACGACGAGTGGCCCTGACCTGCTGCTGCTGCTG 224

QY 61 LeuLeuIleGlyLeuAlaLeuAlaLeuLeuLeuPheGlnTyrTyrGlnLeuSerAsn 80
 DB 225 CTGCTGATAGGCTGGCAGCCCTGGGGCTTTTGTGTTTTCAGTACTACCACTCTCCAAT 284

QY 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
 DB 285 ACTGTCAGACACCATTTCTCAATGGAGAAAGATTAGGAATACGTCCTCCAGAGTTG 344

QY 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120
 DB 345 CAATCTCTCAAGTCCAGATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAA 404

QY 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
 DB 405 CTCTGCTGAGCTGTATAACAAAGCTGGAGCACAGTGCGAGCCCTTGTACAGAACAA 464

QY 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
 DB 465 TGGAAATGGCATGGAGACAATTTGCTACCAAGTTCTATAAGACAGCAAAAGTTGGGAGGAC 524

QY 161 CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
 DB 525 TGTAAATATTCTGCTTAGTGAAACCTACCATGCTGAAGATTAACAACAAGAGAC 584

QY 181 LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu 200
 DB 585 CTGGAATTTGCGCGCTCTCAGAGCTACTCTGAGTTTCTACTCTTATTGGACAGGGCTT 644

QY 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
 DB 645 TTGCGCCCTTGACAGTGCGCAAGCCCTGGCTGTGGATGGATGGAAACCCCTTCTACTTCTGAA 704

QY 221 LeuPheHisIleIleAlaPheValThrSerProArgSerArgAspCysValAlaIleLeu 240
 DB 705 CTGTTCCATATTATATAGATGTCACAGCCCAAGACAGACAGACTGTGTGGCCATCTT 764

QY 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
 DB 765 AATGGAGTATCTTCTCAAGGACTGCAAGAAATTTGAAGCGTTGTCTGTGAGAAAGG 824

QY 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGlyAsp 280
 DB 825 GCAGGAATGGTGAAGCCAGAGAGCCTCCATGTGCCCCCTGAAACATTAGGCGAAGGTGAC 884

RESULT 6
 CR606141
 LOCUS full-length cDNA clone CS0DE006YK19 of Placenta of Homo sapiens (human)
 DEFINITION
 ACCESSION CR606141
 VERSION CR606141.1 GI:50486948
 KEYWORDS HTC; CNSLT cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (Bases 1 to 1673)
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Feng Liang Email: fliang@lifetech.com URL:
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue
 Redwood City, CA 94063
 Genoscope.
 Direct Submission
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
 - Web: www.genoscope.cns.fr)
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with NotI and cloned
 into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 Location/Qualifiers
 1..1673
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DE006YK19"
 /tissue_type="Placenta"
 /plasmid="pCMVSPORT_6"

ORIGIN
 Alignment Scores:
 Pred. No.: 1,628-150 Length: 1673
 Score: 1490.00 Matches: 276
 Percent Similarity: 99.64% Conservative: 0
 Best Local Similarity: 99.64% Mismatches: 1
 Query Match: 98.81% Indels: 0
 DB: 3 Gaps: 0

US-10-689-742-160 (1-280) x CR606141 (1-1673)

QY 4 LysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMetSerLeuHis 23
 DB 2 AAGTACAGACGACGAGGACATGCTGGATGATGGGACACCACTAGCGCTGCAT 61

QY 24 SerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHisArgAlaPro 43
 DB 62 TCTCAAGGCTCTGCCAACCTCGGATCCAGAGCCCGGCGCACAGACAGAGGCTCCC 121

QY 44 SerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuValLeuLeu 63
 DB 122 TCTTCAACGTGGCGACACCATGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGATA 181

QY 64 GlyLeuAlaAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsnThrGlyGln 83
 DB 182 GGGCTGGGACGCTGGGCTTTTGTGTTTTCAGTACTACCACTCTCCATATCTGCTCAA 241

QY 84 AspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeuGlnSerLeu 103
 DB 242 GACACCAATTTCTCAATGGAGAAAGATTAGGAATAGCTCCCAAGAGTTGCAATCTCTT 301

QY 104 GlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLysLeuCysArg 123
 DB 302 CAAGTCCAGATATATAAGCTTGCAGGAAGTCTGCGAGCATGTGGCTGAAACATCTGCTG 361

QY 124 GluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGlnTrpLysTrp 143
 DB 362 GAGCTGTATATACAAAGCTGGAGCACACAGGTGACGCCCTTGTACAGAACAAATGGAATG 421

QY 144 HisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAspCysLysTyr 163
 DB 422 CATGGAGACAAATTTGCTACAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAATAT 481

QY 164 PheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAspLeuGluPhe 183

Db 482 TTCTGCCTTAGTGAATACTTACCATGCTGAAGATAAACAACAAGAACCTGGAAATT 541
 Qy 184 AlaAlaSerGlnSerTyrSerCluPhePheTyrSerTyrTyrThrGlyLeuLeuArgPro 203
 Db 542 GCCGCGTCTCAGAGCTACTCTGAGTTTCTTACTCTTATTTGACAGGCGCTTTGGCGCCT 601
 Qy 204 AspSerGlyLysAlaTyrLeuTyrMetAspGlyThrProPheThrSerGluLeuPheHis 223
 Db 602 GACAGTGGCAGGCGCTGGCTGGATGGATGGAAACCCCTTTCACCTTCTGAACTGTTCAT 661
 Qy 234 llellelleAspValThrSerProArgSerArgAspCysValAlaIleLeuAsnGlyMet 243
 Db 662 ATTATATAGATGTCAACAGCCCAAGAAGCAGAGACTGTGTGCCCATCTTAAATGGGATG 721
 Qy 244 ilePheSerLysAspCysGluLeuLysArgCysValCysGluArgArgAlaGlyMet 263
 Db 722 ATCTTCTCAAGGACTGCAAGAAATTGAAGCGTTGTCTGTGAGAGAGGCGCAGGAATG 781
 Qy 264 ValLysProGluSerLeuHisValProGluThrLeuGlyGluGlyAsp 280
 Db 782 GTGAAGCCAGAGAGCGCTCCATGCTCCCTGAAACATTAGGCGAAGGTGAC 832

RESULT 7
 CR619172 1747 bp mRNA linear HTC 21-JUL-2004
 LOCUS full-length cDNA clone CSODI067YK14 of Placenta Cot 25-normalized
 DEFINITION of Homo sapiens (human).

ACCESSION CR619172

VERSION CR619172.1 GI:50499979

KEYWORDS HTC; CNSLT cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue

2 (bases 1 to 1747)

Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr

- Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

location/Qualifiers

1. 1747

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODI067YK14"

/tissue_type="Placenta Cot 25-normalized"

/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:

Pred. No.: 2,11e-149 Length: 1747

Score: 1480.00 Matches: 278

Percent Similarity: 94.56% Conservat: 0

Best Local Similarity: 94.56% Mismatches: 2

Query Match: 98.14% Indels: 14

DB: 3 Gaps: 1

US-10-689-742-160 (1-280) x CR619172 (1-1747)

Qy 1 MetGlnAlaLysTyrSerThrArgAspMetLeuAspAspGlyThrMet 20

Db 40 ATCAGGCCAAGTACAGCAGCACCGAGGACATGCTGGATGATGATGGGGACACCACTG 99
 Qy 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40
 Db 100 AGCCTGCATTCTCAAGGCTCTGCCACAACCTGGCATCCAGAGCCCGCGCAGAGCAC 159
 Qy 41 ArgAlaProSerSerThrTyrArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal 60
 Db 160 AGGGCTCCCTCTTCAACGTGGCAGCAGTGGCCCTGACCCCTGCTGACTTTGTGCTTGGTG 219
 Qy 61 LeuLeuIleGlyLeuAlaAlaLeuGlyLeuLeu ----- 71
 Db 220 CTGCTGATAGGCTGGCAGCCCTGGGGCTTTTGTAAGTCTGCGCTCTGACCTGGGGGA 279
 Qy 72 ----- PhePheGlnTyrTyrGlnLeuSerAsnThrGlyGlnAspThrIle 86
 Db 280 GGATCCTCTGTTCCCAAGTTTTTTTCAGTACTACCAAGCTCTCCTCAATACGACCACTT 339
 Qy 87 SerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeuGlnSerLeuGlnValGln 106
 Db 340 TCTCAATAGGAAGAAAGATTAGGAATACGTCCTCCCAAGAGTTGCAATCTCTTCAAGTCCAG 399
 Qy 107 AsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLysLeuCysArgGluLeuTyr 126
 Db 400 AATATAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAACTCTGCTGAGCTGTAT 459
 Qy 127 AsnLysAlaGlyAlaHisArgCysSerProCysThrGluGlnTyrLysTrpHisGlyAsp 146
 Db 460 AACAAAGCTGGAGCACACACAGGTGCAGCCCTTTGTATCAGAAACAATGGAATATGGCATGGAGAC 519
 Qy 147 AsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAspCysLysTyrPheCysLeu 166
 Db 520 AATTGCTACCAAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAATATTTCTGCTTT 579
 Qy 167 SerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAspLeuGluPheAlaIleSer 186
 Db 580 AGTGAAGAACTCTACCAGTCTGAAGATAAACAACAAGAACCTGGAATTTGGCCGCTCT 639
 Qy 187 GlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeuLeuArgProAspSerGly 206
 Db 640 CAGAGCTACTCTGAGTTTTTTCTACTCTTATTTGGACAGGGCTTTTTCGCGCCCTGACAGTGGC 699
 Qy 207 LysAlaTyrLeuTyrMetAspGlyThrProPheThrSerGluLeuPheHisIleIle 226
 Db 700 AAGCCTGGCTGTGATGATGGATGGAAACCCCTTCTGAACTGTTCCATATATATA 759
 Qy 227 AspValThrSerProArgSerArgAspCysValAlaIleLeuAsnGlyMetIlePheSer 246
 Db 760 GATGTCACAGCCCAAGAACGACAGACTGTGTGGCCATCCTTAATGGGATGATCTTCTCA 819
 Qy 247 LysAspCysLysGluLeuLysArgCysValCysGluArgArgAlaGlyMetVallyspPro 266
 Db 820 AAGGACTGCAAGAAATTGAAGCGTTGTCTGTGAGAGAAGCGCAGGAATGGTGAAGCCA 879
 Qy 267 GluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280
 Db 880 GAGAGCTTCCATGTCCCCCTGAAACATTAGCGCAAGGTGAC 921

RESULT 8

CR598502

LOCUS full-length cDNA clone CSODI044YF02 of Placenta Cot 25-normalized

DEFINITION of Homo sapiens (human).

ACCESSION CR598502

VERSION CR598502.1 GI:50479309

KEYWORDS HTC; CNSLT cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1759)

Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue
 2 (bases 1 to 1759)
 Genoscope.
 Direct Submission
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.

FEATURES
source

Location/Qualifiers
 1..1759
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS01044YF02"
 /tissue type="placenta Cot 25-normalized"
 /plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:

Pred. No.: 5,25e-147 Length: 1759
 Score: 1458.00 Matches: 278
 Percent Similarity: 88.82% Conservative: 0
 Best Local Similarity: 88.82% Mismatches: 2
 Query Match: 96.68% Indels: 34
 DB: 3 Gaps: 1

US-10-689-742-160 (1-280) x CR598502 (1-1759)

QY 1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspGlyAspThrThrMet 20
 DB 1 ATGCGAGCCCAAGTACAGCAGCAGGAGCATGCTGGATGATGGGACACCACTG 60
 QY 21 SerLeuHisSerGlnAlaSerAlaThrArgHisProGluPro----- 35
 DB 61 AGCCTGCATTCTCAAGGCTCTGCCACAACTCGGCATCCAGAGCCCGCGGCACAGCTGG 120
 QY 35 ----- 35
 DB 121 ACTAGAGTGGCAGCATCAGCACTCACTGCAGCCTTGACCTCCCTCAAGCAATCCTC 180
 QY 36 -----ArgArgThrGluHisArgAlaProSerSerThrTrp 47
 DB 181 CCACCTCAGCCTTCTGAGTAGTGGCACT-ACAGAGCAGAGGCTCCCTCTTCAACGTGG 239
 QY 48 ArgProValAlaLeuThrLeuLeuThrLeuCysLeuValLeuLeuLeuAla 67
 DB 240 CGACCAAGTGGCCCTGACCTCTGACTTTGCTGGTCTGCTGATAGGCTGGCAGCC 299
 QY 68 LeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsnThrGlyGlnAspThrIleSer 87
 DB 300 CTGGGGCTTTGTTTTCAGTACTACCAAGCTCTCAATCTGCTCAAGACACCACTTCT 359
 QY 88 GlnMetGluLysArgLeuGlyAsnThrSerGlnGlnLeuGlnSerLeuGlnValGlnAsn 107
 DB 360 CAAATGGGAAGAAGATTAGGAATAACGTCCTCCCAAGAGTTGCAATCTCTTCAAGTCCAGAT 419
 QY 108 IleLysLeuAlaGlySerLeuGlnHisValAlaGluLysLeuCysArgGluLeuTrpAsn 127
 DB 420 ATAAAGCTTGGAGGAAGCTCGAGCATGGGCTGAAAACTCTGCTGAGCTGTATATAC 479
 QY 128 LysAlaGlyValAlaHisArgCysSerProCysThrGluGlnTrpLysTrpHisGlyAspAsn 147
 DB 480 AAGCTGGAGCACACAGGTGGAGCCCTGTACAGAACATGGAATGCATGAGACCAAT 539
 QY 148 CysTyrGlnPheTyrLysAspSerLysSerTrpGluAspCysLysTyrPheCysLeuSer 167

DB 540 TGCTACCAAGTTCTATAAAGACAGCAAAAGTTGGAGGACTGTAAATATTTTTCGCCTTAGT 599
 QY 168 GluAanSerThrMetLeuLysIleAsnLysGlnGluAspLeuGluPheAlaIleAsnGln 187
 DB 600 GAAACTCTACCATGCTGAAGATAAACAACAAGAGACTTGGATTTTCCCGGCTCTCAG 659
 QY 188 SerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeuLeuArgProAspSerGlyLys 207
 DB 660 AGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGGCCCTGACAGTGGCAAG 719
 QY 208 AlaTrpLeuTrpMetAspGlyThrProPheThrSerGluLeuPheHisIleIleAsp 227
 DB 720 GCTCGCTGTGATGATGGAACCCCTTCACTTCTGAACCTGTTCATATTAATATAGAT 779
 QY 228 ValThrSerProArgSerArgAspCysValAlaIleLeuAsnGlyMetIlePheSerLys 247
 DB 780 GTCACCAAGCCCAAGAGCAGACACTGTGTGGCCATCTTAATGGCATGATCTTCTCAAG 839
 QY 248 AspCysLysGluLeuLysArgCysValCysGluAArgAlaGlyMetValLysProGlu 267
 DB 840 GACTGCAAGAAATTGAAGCGTTGTCTGTGTGAGAGAGGCGAGGAATGTTGAAGCCAGAG 899
 QY 268 SerLeuHisValProGluThrLeuGlyGluGlyAsp 280
 DB 900 AGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGAC 938

RESULT 9

BX358357 927 bp mRNA linear EST 08-APR-2004
 LOCUS BX358357 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS01036YF20 5-PRIME, mRNA sequence.

ACCESSION

BX358357

VERSION

BX358357.2 GI:46289437

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 927)
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

AUTHORS

Full-length cDNA libraries and normalization

TITLE

Unpublished (2001)

JOURNAL

On May 5, 2003 this sequence version replaced gi:30370217.

COMMENT

Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

FEATURES

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 6541.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CS01036YF20&c=6541.r.
 Location/Qualifiers
 1..927
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS01036YF20"
 /tissue type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores: 3.6e-146 Length: 927
 Pred. No.: 1446.50 Matches: 271
 Score:

Percent Similarity: 97.84% Conservatives: 1
 Best Local Similarity: 97.48% Mismatches: 5
 Query Match: 95.92% Indels: 1
 DB: 5 Gaps: 1

US-10-689-742-160 (1-280) x BX358357 (1-927)

QY 1 MetGlnAlaLysTyrSerThrArgAspMetLeuAspAspGlyAspThrThrMet 20
 Db 10 ATGAGGCAAGTACAGCAGCAGGACATGCTGGATGATGATGGGACACACCATG 69
 QY 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40
 Db 70 AGCTTGCATTTCTCAAGGCTCTGCCAACTCGGCATCCAGAGCCCGCGCACAGAGCAC 129
 QY 41 ArgAlaProSerSerThrTTPArgProValAlaLeuThrLeuLeuLeuCysLeuVal 60
 Db 130 AGGGCTCCCTCTTCAAGCTGGCGACAGTGGCCCTGACCTGCTGACTTTGTGCTGTGTG 189
 QY 61 LeuLeuLeGlyLeuAlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsn 80
 Db 190 CTGCTGATAGGCTGGCAGCCCTGGGCTTTTGTGTTTTTTCAGTACTACCGCTCTCCAAT 249
 QY 81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
 Db 250 ACTGCTCAAGACACCATTTCTCAATGGAAGAAAGATTAGGAAATACGTCCTCAAGAGTTG 309
 QY 101 GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaLagLys 120
 Db 310 CAATCTTCAAGTCCAGATATAAAGCTTCGAGGAAGTCTGCAGCATGTGGCTGGAANA 369
 QY 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
 Db 370 CTCTGCTGAGCTGTATACAAAGCTGGAGCACACAGCTGCAGCCCTGTGTACAGAACAA 429
 QY 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
 Db 430 TCGAAATTTGCGGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTTTATTGGACAGGGCTT 609
 QY 201 LeuArgProAspSerGlyAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
 Db 610 TTGCGCCCTGACAGTGGCAAGCCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAA 669
 QY 221 LeuPheHisIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu 240
 Db 670 CTGTTCCATATTATATAGATGTACACAGCCCAAGACAGAGACTGTGTGGCCATCTTT 729
 QY 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
 Db 730 AATGGAGATCTTCTCAAGGACTGCAAGAAATTGAAGCTGTGTCTGTGAGAGAGG 789
 QY 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGlu 278
 Db 790 GCAGGAATGGTGAAG---CAGAGAGCTCCATGTCTCCCTCGAAACATTAGGCGAG 840

RESULT 10
 BX391810/C
 LOCUS BX391810 914 bp mRNA linear EST 28-APR-2004
 DEFINITION BX391810 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1081YG24 3-PRIME, mRNA sequence.
 ACCESSION BX391810
 VERSION BX391810.1 GI:30615587
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 914)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 6541.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS08A1029ZA09_CS02753_l&c=6541.r

FEATURES
 source

Location/Qualifiers
 1. 914

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1081YG24"
 /tissue type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 1,09e-145 Length: 914
 Score: 1442.00 Matches: 267
 Percent Similarity: 98.89% Conservative: 0
 Best Local Similarity: 98.89% Mismatches: 3
 Query Match: 95.62% Indels: 0
 DB: 5 Gaps: 0
 US-10-689-742-160 (1-280) x BX391810 (1-914)

QY 11 MetLeuAspAspGlyAspThrThrMetSerLeuHisSerGlnAlaSerAlaThrThr 30
 Db 912 ATGCTGGATGATGATGGGACACACCATGAGCTGCATTTCTCAAGCTCTGCACAACT 853
 QY 31 ArgHisProGluProArgArgThrGluHisArgAlaProSerSerThrTrpArgProVal 50
 Db 852 CGGCATCCAGAGCCCGCGCACAGACACAGGGCTCCCTCTTCAACGTGGCGACCACTG 793
 QY 51 AlaLeuThrLeuLeuThrLeuCysValLeuLeuLeuGlyLeuAlaLeuGlyLeu 70
 Db 792 GCCCTGACCCCTGCTGACTTTGTGCTGTGCTGATAGGGCTGGCAGCCCTGGGGCTT 733
 QY 71 LeuPhePheGlnTyrTyrGlnLeuSerAsnThrGlyGlnAspThrIleSerGlnMetGlu 90
 Db 732 NTGTTTTTTCAGTACTACCGCTCTCCAATACTGTGTCAAGACACCAATTTCTCAATGAA 673
 QY 91 GluArgLeuGlyAsnThrSerGlnGluLeuSerLeuGlnValGlnAsnIleLysLeu 110
 Db 672 GAAAGATTAGGAAATACGTCCTCAAGAGTTGCAATCTCTTCAAGTCCAGAAATATAAGGTT 613
 QY 111 AlaGlySerLeuGlnHisValAlaGlyLysLeuCysArgGluLeuTyrAsnLysAlaGly 130
 Db 612 GCAGAGAGTCTGACAGCATGTGGCTGAAAAAACTCTGTGTGAGCTGTATACAAAGCTGGA 553
 QY 131 AlaHisArgCysSerProCysThrGluGlnTrpLysTrpHisGlyAspAsnCysTyrGln 150
 Db 552 GCACAGGTGCAGCCCTTTGTACAGAAACATGGAATGGCATGGAGACAAATTGCTACCAG 493
 QY 151 PheTyrLysAspSerLysSerTrpGluAspCysLysTyrPheCysLeuSerGluAsnSer 170

Db 492 TTCTATTAAGACAGCAGCAAGTTGGAGGACTGCTAAATATTTCTGCTTAGTGCAAACTCT 433
 Qy 171 ThrMetLeuLysIleAsnLysGlnGluAspLeuGluPheAlaAlaSerGlnSerTyrSer 190
 Db 432 ACCATGCTGAGATAAACAACAGAGACCTGGAATTTGCCGCTCTCAGAGCTACTCT 373
 Qy 191 GluPhePheTyrSerTyrTTPThrGluLeuLeuArgProAspSerGlyLysAlaTTPLeu 210
 Db 372 GAGTTTTTCTACTCTATTATGGACAGGCTTTTGGCCCTGACAGTGGCAAGCCCTGGCTG 313
 Qy 211 TTPMetAspGlyThrProPheThrSerGluLeuPheHisIleIleAspValThrSer 230
 Db 312 TGGATGGATGGAAACCCCTTCTACTCTGAACTGTTCCATATATATATATGATGTCACAGC 253
 Qy 231 ProArgSerArgAspCysValAlaIleLeuAsnGlyMetIlePheSerLysAspCysLys 250
 Db 252 CCAAGAAGCAGAGACTGTGTGGCCATCCTTAATGGATGATCTTCTCAAGGACTGCAAA 193
 Qy 251 GluLeuLysArgCysValCysGluArgAlaGlyMetValLysProGluSerLeuHis 270
 Db 192 GAATTTGAAGCGTGTGTCTGTGAGAGAAGGCGAGGAATGTTGAAGCCAGAGAGCTCCAT 133
 Qy 271 ValProGluThrLeuGlyGluGlyAsp 280
 Db 132 GTCCCCCTGAAACATTAGGCGAAGTGAC 103

RESULT 11
 AL541315 1049 bp mRNA linear EST 24-MAR-2004
 LOCUS AL541315 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0D8006YK19
 DEFINITION 5-PRIME, mRNA sequence.
 ACCESSION AL541315
 VERSION AL541315.3 GI:45716909
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1049)
 Li.W.B., Gruber.C., Jessee.J., and Polayes.D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:30545374.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqrefgenoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 6541.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?8=CS0D8006AF10QPl&c=6541.r.
 Location/Qualifiers
 1..1049
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D8006YK19"
 /tissue_type="PLACENTA"
 /clone_lib="Homo sapiens PLACENTA"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

FEATURES

source
 1..1049
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D8006YK19"
 /tissue_type="PLACENTA"
 /clone_lib="Homo sapiens PLACENTA"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 1049
 Score: 1438.50 Matches: 275

Percent Similarity: 99.28% Conservative: 0
 Best Local Similarity: 99.28% Mismatches: 2
 Query Match: 95.39% Indels: 2
 DB: 1 Gaps: 0

US-10-689-742-160 (1-280) x AL541315 (1-1049)

Qy 4 LysTyrSerSerThrArgAspMetLeuAspAspGlyAspThrThrMetSerLeuHis 23
 Db 2 AAGTACAGCAGCAGGAGGACATGCTGATGATGATGGGACACACCATGAGCGCTGCAT 61
 Qy 24 SerGlnAlaSerAlaThrArgHisProGluProArgArgThrGluHisArgAlaPro 43
 Db 62 TCTCAAGCCTCTGCCCAACTCGGCATCCAGAGCCCGGCACAGACAGAGCGGCTCCC 121
 Qy 44 SerSerThrTTPArgProValAlaLeuThrLeuLeuThrLeuCysLeuValLeuLeuIle 63
 Db 122 TCTTCAACGTGGGACCACTGACCTGACCTGCTGACTTGTGCTGGTGTGCTGATA 181
 Qy 64 GlyLeuAlaAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsnThrGlyGln 83
 Db 182 GGGCTGGCAGCCCTGGGGCTTTTGTGTTTTTTCAGTACTACCACTCTCCAATACTGGTCAA 241
 Qy 84 AspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeuGlnSerLeu 103
 Db 242 GACACCATTTCTCAAAATGGAAGAAGATTAGAAATACGTCCCAAGATTGCATCTCTT 301
 Qy 104 GlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLysLeuCysArg 123
 Db 302 CAAGTCCAGATATATAAGCTTGCAGGAAGTCTGCAGCAGTGTGGCTGAAAAACTCTGTCT 361
 Qy 124 GluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGlnTTPlysTTP 143
 Db 362 GAGCTGTATAACAAAGCTGGGACACACAGGTGCAGCCCTTGTACAGAAACAATGGAAATGG 421
 Qy 144 HisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTTPGluAspCysLysTyr 163
 Db 422 CATGGAGACAATTGCTACAGTTCTATAAGACAGCAAAAGTTGGGAGAGACTGTAAATAT 481
 Qy 164 PheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAspLeuGluPhe 183
 Db 482 TCTGCTCTAGTGAACACTCTACCATGCTGAAGATATAACAAACAGAGACCTGGAAATTT 541
 Qy 184 AlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTTPThrGlyLeuLeuArgPro 203
 Db 542 GCCGCTCTCAGAGCTACTCTGAGTTTCTTACTCTTATTTGACAGGCGCTTTTGGCCCT 601
 Qy 204 AspSerGlyLysAlaTTPLeuTTPMetAspGlyThrProPheThrSerGluLeuPheHis 223
 Db 602 GACAGTGGCAAGGCTGGCTGTGGATGATGGAACCCCTTTCACCTCTCGAACTGTTCAT 661
 Qy 224 IleIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeuAsnGlyMet 243
 Db 662 ATTATATAGATGTGCACAGCCCAAGAGCAGAGACTGTGTGGCCATCTCTTAATGGATG 721
 Qy 244 IlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgAlaGlyMet 263
 Db 722 ATCTTCTCAAGGACTGCAAGAAATTGAAGCGTTGTGTCTGTGAGAGAGGCGGAGAAATG 781
 Qy 264 VallysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280
 Db 782 GTGAAGCA-GAGAGCCTCCATGT-CCCCCTGAAACATTAGGCGAAGGTGAC 830

RESULT 12

EX324788
 LOCUS BX324788 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0D1049YB09 5-PRIME, mRNA sequence.
 ACCESSION BX324788
 VERSION BX324788.2 GI:46271524
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1001)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:30336406.

CONTACT: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dr) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6541.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0A1049CA05QPI&c=6541.r.

FEATURES

source
1..1001
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1049YB09"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dr)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 1001
Score: 1431.50 Length: 1001
Percent Similarity: 98.56% Matches: 274
Best Local Similarity: 98.56% Mismatches: 4
Query Match: 94.93% Indels: 2
DB: 5 Gaps: 0
US-10-689-742-160 (1-280) x BX324788 (1-1001)
Qy 1 MetGlnAlaLysTyrSerThrArgAspMetLeuAspAspGlyAspThrThrMet 20
Db 45 ATGAGGCCAAGTACAGCAGCAGGACATGCTGGATGATGATGGGACACACCATG 104
Qy 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgThrGluHis 40
Db 105 AGCCTGCATTCTCAAGGCTCTGCCCAACTCGGCATCCAGAGCCCGCGCACAGAGCAC 164
Qy 41 ArgAlaProSerSerThrTrrArgProValAlaLeuThrLeuLeuLeuVal 60
Db 165 AGGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCCCTGCTGCTGGTG 224
Qy 61 LeuLeuLeuGlyLeuAlaLeuGlyLeuLeuPheGlnTyrTyrGlnLeuSerAsn 80
Db 225 CTGCTGATAGGCTGGCAGCCCTGGGGCTTTGTTTTCAGTACTACCACTCTCCAT 284
Qy 81 ThrGlyGlnAspThrIleSerGlnMetGluArgLeuGlyAsnThrSerGlnGluLeu 100
Db 285 ACTGGTCAAGACACCATTTCTCAATGGAAGAAATAGGAAATACCTCCCAAGAGTTG 344
Qy 101 GlnSerLeuGlnValGlnAsnIleLeuAlaGlySerLeuGlnHisValAlaGluLys 120
Db 345 CAATCTCTCAAGTCCCAATATAAGCTTGAGGAAGTCTGCAGCATGTGGCTGAAAAA 404
Qy 121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140
Db 405 CTCTGCTGAGCKGTATAACAAGCTGGAGCACACAGTGCAGCCCTTGTACAGACAA 464
Qy 141 TrpLysTrpHisGlyAspAsnCysTrrGlnPheTyrLysAspSerLysSerTrpGluAsp 160

Db 465 TGGAAATGGCATGGAGACAATGTTACCAGTTCTATAAAGACAGACAAAGTTGGAGGAC 524
Qy 161 CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGluGluAsp 180
Db 525 TGTAAATATTCTCGCCCTTAGTGAAGAACTCTACCAGTCTGAAGATAAACAAGAGAC 584
Qy 181 LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu 200
Db 585 CTGGAATTTGCGCGTCTCAGAGCTACTCTGAGTTTCTTACTCTTATTGGACAGGGCTT 644
Qy 201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220
Db 645 TTGGCCCTCAGACAGTGGCAAGCCCTGGCTGTGGATGATGAGACCCCTTTCACTTCTGAA 704
Qy 221 LeuPheHisIleIleLeuAspValThrSerProArgSerArgAspCysValAlaIleLeu 240
Db 705 CTGTTCCATATTATAATAGATGTCAACGCCCAAGAGCAGAGACTGTGTGGCATCTT 764
Qy 241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArg 260
Db 765 AATGGATGATCTTCTCAAGGACTGCAAGAAATGAAGCGTTGTGTGTGAGAGAGG 824
Qy 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGlu 278
Db 825 GCAGGAATGGTGAAGCA-GAGAGCCTCCATGT-CCCCCTGAACATTAGGCGAG 876
RESULT 13
BX399696 958 bp mRNA linear EST 29-APR-2004
LOCUS BX399696 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1081YG24 5-PRIME, mRNA sequence.
ACCESSION BX399696
VERSION BX399696.2 GI:46873746
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 958)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 13, 2003 this sequence version replaced gi:30617945.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dr) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6541.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1081BD12QPI&c=6541.r.

FEATURES

source

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/clone="CS0D1081YG24"
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/note="1st strand cDNA was primed with a NotI-oligo (dr)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 1.53e-143 Length: 958
Score: 1422.50 Matches: 269
Percent Similarity: 98.53% Conservative: 0


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Qy 147 AenCysTyrGlnPheTyrLysAspSerLysSerTTPGluAspCysLysTyrPheCysLeu 166
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Db 532 AATTGCTACCAAGTCTTATAAGACAGCAAAAGTTGGAGGACTGTAATATATTTTCGCCCTT 591
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Qy 167 SerGluAenSerThrMetLeuLysLeuAenLysGlnGluAspLeuGluPheAlaAlaSer 186
    |||||
Db 592 AGTGAANAACCTTACCATGCTGAAGATAAACCAACAAAGAACCTTGAATTTGGCCGCTCT 651
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Qy 187 GlnSerTyrSerGluPhePheTyrSerTyrTTPThrGlyLeuLeuArgProAspSerGly 206
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Qy 207 LysAlaTTPLeuTTPMetAspGlyThrProPheThrSerGluLeuPheHisIleIleIle 226
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Db 712 AAGGCTGGCTGTGGATGGATGGAAAC-CCTTTCACCTTCTGAACTTCCATATATATAATA 770
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Qy 227 AspValThrSerProArgSerArgAspCysValAlaIleLeuAenGlyMetIlePheSer 246
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Db 771 GATGTCAACAGCCCAAGAACAGACAGACTGTGTGGCCATCTTAAATGGCATGATCTTCTCA 830
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Qy 247 LysAspCysLysGluLeuLysArgCysValCysGluArgArgAlaGlyMetValLysPro 266
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Db 831 AAGGACTCAAGAAGATTCGAAGCGTTGTCTGTGAGAGAGGGCAGGAATGTTGAAGCA- 889
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Qy 267 GluSerLeuHisValProGluThrLeuGlyGlu 278
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Db 890 GAGAGCTCCATGTCCTCCCTGAAACATTAAGSGAG 925
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RESULT 15

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BX339075
LOCUS      BX339075 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1067YK14 5-PRIME, mRNA sequence.
ACCESSION BX339075
VERSION   BX339075.2 GI:46270291
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 964)
            Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
            Full-length cDNA libraries and normalization
            Unpublished (2001)
            On May 2, 2003 this sequence version replaced gi:30335767.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            6541.r

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For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CS0D1067BF07QPI&c=6541.r>.

FEATURES

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ORIGIN

Search completed: October 8, 2005, 04:08:00
 Job time : 4109.18 secs

Alignment Scores:

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Pred. No.:      2.19e-140      Length:      964
Score:           1393.50      Matches:      265
Percent Similarity: 92.66%      Conservative: 0
Best Local Similarity: 92.66%      Mismatches: 6
Query Match:     92.41%      Indels: 15
DB:              5          Gaps: 2

US-10-689-742-160 (1-280) x BX339075 (1-964)

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Db 40 ATGCAGGCCCAAGTACAGCAGCAGCAGGACATGCTGGATGATGATGGGGACACACCACATG 99
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Qy 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40
    |||||
Db 100 AGCTTGATTTCTCAAGGCTCTGCCCAAACTCGGCATCCAGAGCCCCGGCGGCAGAGCAC 159
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Qy 41 ArgAlaProSerSerThrTTPArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal 60
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Db 160 AGGCTCCCTCTTCAACGTGGCGACCAAGTGGCCCTGACCCCTGCTGCTTTGCTTGGTG 219
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Qy 61 LeuLeuIleGlyLeuAlaAlaLeuGlyLeuLeu----- 71
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Db 220 CTGCTGATAGGGCTGGCAGGCCCTGGGGCTTTTGTGTAAAGTCTGCGCTCTGACCTGGGGGA 279
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Qy 72 -----PhePheGlnTyrTyrGlnLeuSerAenThrGlyGlnAspThrIle 86
    |||||
Db 280 GGATCCTCGTTCCAAAGTTTTTTCAGTACTACAGCTCTCCAATACTGGTCAAGACACCAATT 339
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Qy 87 SerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeuGlnSerLeuGlnValGln 106
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Qy 107 AsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLysLeuCysArgGluLeuTyr 126
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Db 400 AATAAAGCTTGCGAGGAAGTCTGCAGCATGTGGCTGAAAAAACTCTCTCGTGAGCTGTAT 459
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Qy 127 AsnLysAlaGlyAlaHisArgCysSerProCysThrGluGlnTTPLysTTPHisGlyAsp 146
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Db 460 AACAAAGCTGGAGCACACAGGTGCGCCCTTGTACAGAACATGGAATGGCATGGAGAC 519
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Qy 147 AsnCysTyrGlnPheTyrLysAspSerLysSerTTPGluAspCysLysTyrPheCysLeu 166
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Qy 167 SerGluAenSerThrMetLeuLysIleAsnLysGlnGluAspLeuGluPheAlaAlaSer 186
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Qy 187 GlnSerTyrSerGluPhePheTyrSerTyrTTPThrGlyLeuLeuArgProAspSerGly 206
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Qy 227 AspValThrSerProArgSerArgAspCysValAlaIleLeuAenGlyMetIlePheSer 246
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Qy 247 LysAspCysLysGluLeuLysArgCysValCysGluArgArgAlaGlyMetValLysPro 266
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